AMENDMENTS TO THE SPECIFICATION

Please **AMEND** page 1, lines 4-7 in the specification, as follows:

This application claims the benefit of U.S. Provisional Application Nos. 60/491,258 filed July 31,2003, 60/493,767 filed August 11, 2003, 60/496,908 filed August 22, 2003, and 60/501,832 filed September 11, 2003, and of International Application PCT/US04/02064, filed January 28, 2004, which are hereby incorporated by reference in their entirety.

Please **REPLACE** Table 1, pages 20-25 in the specification, as follows:

TABLE 1

THE OPEN READING FRAMES OF VACCINIA VIRUS

Gene[a]	Translation Start	Translation Stop[b]	Size aa	Size M_r[c]	Characteristics[d]	References
C23L*	5008	4277	244	26.4	Nonessential; B29R Acidic[e] (4.2)	Perkus, et al. (1990b)
C22L*	6113	5748	122	13.6	Nonessential; B28R Hydrophobic N-terminus	Perkus, et al. (1990b)
C21L*	6815	6477	113	13.4	Nonessential; B27R	Perkus, et al. (1990b)
C20L*	7132	6824	103	12.5	Nonessential; B26R Basic (9.0)	Perkus, et al. (1990b)
C19L*	7856	7080	259	30.5	Nonessential; B25R Hydrophobic N-terminus	Perkus, et al. (1990b)
C18L*	8693	8244	150	17.5	Nonessential; B24R Acidic (4.8)	Perkus, et al. (1990b)
C17L*	9947	8790	386	44.9	Nonessential; B23R	Perkus, et al. (1990b)
C16L*	10539	9997	181	21.0	Nonessential; B22R	Perkus, et al. (1990b)
C15L*	11153	10881	91	10.5	Nonessential; B21R	Perkus, et al. (1990b)
C14L	12212	11967	82	9.3	Nonessential Basic (9.2)	Perkus, et al. (1990b)
C13L	12510	12316	65	7.4	Nonessential Acidic (4.0)	Perkus, et al. (1990b)
C12L	13733	12675	353	40.4	Serine Protease Inhibitor Nonessential Acidic (4.8)	Kotwal and Moss (1988b) Perkus, et al. (1990b)
C11R	14178	14603	142	15.8	Growth Factor Nonessential EGF-like type A domain Hydrophobic C-terminus	Blomquist, et al. (1984); Brown, et al. (1985); Reisner (1985) Buller, et al. (1988); Perkus, et al. (1990b)
C10L	15754	14762	331	38.5	Nonessential Acidic (4.5)	Perkus, et al. (1990b)
C9L	18136	16235	634	74.7	Nonessential	Perkus, et al. (1990b); Kotwal and Moss (1988b)
C8L	18733	18182	184	21.6	Nonessential Acidic (4.4)	Kotwal and Moss (1988b); Perkus, et al. (1990b)

C7L	19257	18808	150	18.0	Nonessential	Kotwal and Moss (1988b); Perkus, et al. (1990a,b)
					Host range function	Perkus, et al. (1990a)
C6L	19939	19487	151	17.4	Nonessential	Kotwal and Moss (1988b); Perkus, et al. (1990b)
					Acidic (4.8)	
C5L	20680	20069	204	24.5	Nonessential	Kotwal and Moss (1988b); Perkus, et al. (1990b)
					Acidic (4.8))	
C4L	21693	20746	316	37.2	Nonessential	Kotwal and Moss (1988b); Perkus, et al. (1990b)
C3L	22551	21763	263	28.6	Nonessential	Kotwal and Moss (1988a,b); Perkus, et al. (1990b)
					C4B binding protein homolog; virokine	Kotwal and Moss (1988a)
C2L	24156	22621	512	59.2	Nonessential	Kotwal and Moss (1988b); Perkus, et al. (1990b)
					Hydrophobic N-terminus	
C1L	24900	24229	224	26.4	Nonessential	Kotwal and Moss (1988b); Perkus, et al. (1990b)
					Basic (9.0)	

Reprinted from *Virology*, Vol. 179, S. J. Goebel, G. P. Johnson, M. E. Perkus, S. W. Davis, J. P. Winslow and E. Paoletti, "The Complete DNA Sequence of Vaccinia Virus", pgs. 247-266 (1990), with permission from Elsevier.

TABLE 1—*Continued*

Gene[a]	Translation Start	Translation Stop[b]	Size aa	Size M_r[c]	Characteristics	References
N1L	25240	24890	117	14.0	Nonessential	Kotwal and Moss (1988b); Perkus, *et al.* (1990b)
					Virokine	Kotwal and Moss (1988a)
					Acidic (4.2)	
N2L	25886	25362	175	20.8	Nonessential	Kotwal and Moss (1988a,b); Perkus, *et al.* (1990b)
M1L	27346	25931	472	54.2	Nonessential	Perkus, *et al.* (1990b)
					Homology to K1L	Perkus, *et al.* (1990a)
M2L	27986	27327	220	25.1	Nonessential	Perkus, *et al.* (1990b)
					Hydrophobic N-terminus	
K1L	28975	28124	284	32.6	**Host range function**	Gillard, *et al.* (1986); Perkus, *et al.* (1989)
					Nonessential	Perkus, *et al.* (1990b)
K2L	30313	29207	369	42.3	Serine protease inhibitor	Boursnell, *et al.* (1988)
					Nonessential	Perkus, *et al.* (1990b)
					Basic (9.3)	
K3L	30629	30366	88	10.5	Nonessential	Perkus, *et al.* (1990b)
					Basic (9.3)	
					Translation initiation factor	
K4L	31955	30684	424	48.9	Homology to F13L	Boursnell, *et al.* (1988)
					Nonessential	Perkus, *et al.* (1990b)
K5L	32497	32090	136	15.2	Nonessential	Perkus, *et al.* (1990b)
					Basic (10.2)	
K6L	32764	32522	81	9.1	Nonessential	Perkus, *et al.* (1990b)
K7R	32903	33349	149	17.5	Nonessential	Perkus, *et al.* (1990b)
					Acidic (4.4)	
					Hydrophobic C-terminus	
F1L	34097	33420	226	26.4	Nonessential	Perkus, *et al.* (1990b)
					Acidic (4.4)	
					Hydrophobic C-terminus	

F1L	34097	33420	226	26.4	Nonessential Acidic (4.4) Hydrophobic C-terminus	Perkus, *et al.* (1990b)
F2L	34552	34112	147	16.3	Retroviral protease Nonessential *dUTPase*	Slabaugh and Roseman (1989) Perkus, *et al.* (1990b)
F3L	36018	34579	480	55.7	Nonessential	Perkus, et al. (1990b)
F4L	36988	36032	319	37.0	**Ribonucleotide reductase (small subunit)** Nonessential Acidic (4.6)	Slabaugh, *et al.* (1988) Perkus, *et al.* (1990b)
F5L	37985	37023	321	36.5	Multiply hydrophobic	
F6L	38239	38018	74	8.6	Acidic (4.1)	
F7L	38533	38258	92	11.0	- $(Lys\text{-}Asn)_9$	
F8L	38878	38684	65	7.8	Basic (9.9)	
F9L	39576	38941	212	23.8	Hydrophobic C-terminus	
F10L	40882	39566	439	52.2	Protein kinase 2nd signature	
F11L	41969	40908	354	39.7	-	
F12L	43919	42015	635	73.2	-	
F13L	45079	43964	372	41.8	**Envelope antigen**	Hirt, *et al.* (1986)
F14L	45318	45100	73	8.3	Acidic (2.9)	
F15L	46068	45595	159	18.6	Basic (9.5)	
F16L	46770	46078	231	26.6	Basic (9.6)	
F17R	46833	47135	101	11.3	Basic (9.8)	
E1L	48574	47138	479	55.6	-	
E2L	50784	48574	737	85.9	-	
E3L	51483	50914	190	21.5	Acidic (4.9)	
E4L	52318	51542	259	29.8	Acidic (4.9) *Transcription factor*	

TABLE 1—*Continued*

Gene[a]	Translation Start	Translation Stop[b]	Size aa	Size M_r[c]	Characteristics	References
					(*ts*: C19??)[f]	Condit, *et al.* (1983)
E5R	52395	53387	331	39.1	Basic (9.8)	
E6R	53527	55227	567	66.7	-	
E7R	55314	55811	166	19.5	-	
E8R	55939	56757	273	31.9	Basic (9.3)	
E9L	59787	56770	1006	117.0	**DNA Polymerase**	Earl, *et al.*, 1986
					ts: C42, NG26; PAA[r], Aphidicolin[r]	Traktman, *et al.* (1989b)
					DNA polymerase family B signature	
E10R	59819	60103	95	10.8	-	
E11L	60490	60104	129	14.9	-	
O1L	62477	60480	666	77.6	Leucine Zipper Motif	
O2L	62851	62528	108	12.4	*Glutaredoxin*	
I1L	63935	63000	312	35.8	-	
I2L	64163	63945	73	8.4	Hydrophobic C-terminus	
					Acidic (3.9)	
I3L	64973	64167	269	30.0	-	
I4L	67371	65059	771	87.0	**Ribonucleotide reductase (large subunit)**	Schmitt and Stunnenberg (1988) Tengelsen, *et al.* (1988)
					Nonessential	Perkus, *et al.* (unpublished) Child, *et al.*, (1990)
					Divalent Fe-S ferredoxin binding region signature	
I5L	67637	67401	79	8.7	Basic (9.9)	
I6L	68804	67659	382	43.4	Basic (9.2)	
I7L	70068	68800	423	49.0	-	
I8R	70074	72101	676	77.6	ATP/GTP binding motif A	
G1L	73883	72111	591	67.9	-	
G2R	74209	74868	220	25.7	-	

G3L	74215	73883	111	12.8	Hydrophobic N-terminus	
G4L	75215	74844	124	14.0	Acidic (4.8)	
G5R	75218	76519	434	49.9	Acidic (4.8)	
G6R	76723	77217	165	18.9	-	
G7L	78300	77188	371	41.9	-	
G8R	78331	79110	260	29.9	-	
G9R	79133	80152	340	38.8	Hydrophobic C-terminus	
L1R	80156	80905	250	27.3	Hydrophobic near C-terminus	
L2R	80940	81200	87	10.2	-	
L3L	82245	81196	350	40.6	Multiply hydrophobic	
L4R	82270	83022	251	28.5	Structural protein, VP8	Yang, *et al.* (1988)
L5R	83035	83418	128	14.0	Basic (10.0)	
J1R	83378	83836	153	17.8	-	
J2R	83855	84385	177	20.1	Thymidine kinase	Weir and Moss (1983); Hruby *et al.* (1983)
					Nonessential	Mackett, *et al.* (1982)
					ATP/GTP binding motif A	
J3R	84454	85452	333	15.2	Basic (10.0)	
J4R	85370	85924	185	21.3	RNA Polymerase subunit	Broyles and Moss (1986)
					ts: C7, C20	Hooda-Dhingra, *et al.* (1989); Thompson, *et al.* (1989)
J5L	86403	86005	133	15.2	Hydrophobic C-terminus	
J6R	86510	90367	1286	146.8	RNA Polymerase subunit	Broyles and Moss (1986)
					ts: E8, E13, E72	Ensinger (1987)
					C51, C53, C65	Hooda-Dhingra, *et al.*, (1989); Thompson, *et*

TABLE 1—*Continued*

Gene[a]	Translation Start	Translation Stop[b]	Size aa	Size M_r[c]	Characteristics	References
H1L	90882	90370	171	19.7	Basic (9.6)	
H2R	90896	91462	189	21.5	Hydrophobic N-terminus	
H3L	92442	91471	324	37.5	Multiply hydrophobic	
H4L	94830	92446	795	93.6	-	
H5R	95016	95624	203	22.3	-	
H6R	95628	96569	314	36.7	Basic (10.0)	
					DNA topoisomerase	Shuman and Moss (1987)
H7R	96609	97046	146	16.9	-	
D1R	97093	99624	844	96.7	mRNA capping enzyme (small subunit)	Morgan, *et al.* (1984)
D2L	100026	99589	146	16.9	*ts*: E52, E94	Seto, *et al.* (1987)
D3R	100019	100729	237	28.0	*ts*: C5, C35	Seto, *et al.* (1987)
D4R	100732	101385	218	25.0	-	
D5R	101420	103774	785	90.0	*ts*: C17, C24, E69	Seto, *et al.* (1987)
					ATP/GTP binding motif A	
D6R	103818	105728	637	73.8	Early transcription factor subunit	Broyles and Fesler (1990)
					ts: C46, E93	Seto, *et al.* (1987)
					Hydrophobic N-terminus	
D7R	105758	106240	161	17.9	RNA polymerase subunit	Ahn, *et al.* (1990)
					ts: C21, E45	Seto, *et al.* (1987)
					Acidic (4.5)	
D8L	107120	106209	304	35.3	Carbonic anhydrase	Niles, *et al.* (1986)
					Transmembrane	Niles and Seto (1988)
					Cell surface binding	Maa, *et al* (1990)
					Multiply hydrophobic	
					Basic (9.1)	
D9R	107162	107800	213	25.0	-	
D10R	107800	108543	248	28.9	-	

D11L	110442	108550	631	72.4	NTPase	Rodriguez, *et al.* (1986); Broyles and Moss (1987)
					ts: C36, C50, E17	Seto, *et al.* (1987)
					Basic (9.0)	
D12L	111340	110480	287	33.4	mRNA capping enzyme (small subunit)	Niles, *et al.* (1989)
D13L	113026	111374	551	61.9	*ts*: C33, C43, E101	Seto, *et al.* (1987)
					Rifampicin resistance	Tartaglia and Paoletti (1985); Baldick and Moss (1987)
					Acidic (5.0)	
A1L	113502	113053	150	17.0	-	
A2L	114197	113526	224	26.3	-	
A3L	116372	114441	644	72.6	Major core protein P4b	Rosel and Moss (1985)
A4L	117270	116428	281	30.8	Acidic (4.6)	
A5R	117308	117799	164	19.0	Acidic (4.2)	
A6L	118917	117802	372	43.1	-	
A7L	121073	118944	710	82.3	Early transcription factor subunit	Gershon and Moss (1990)
A8R	121127	121990	288	33.6	-	
A9L	122285	121989	99	11.1	-	
A10L	124961	122289	891	102.3	Major core protein P4a	Van Meir and Wittek (1988)
A11R	124976	125929	318	36.1	Hydrophobic C-terminus	
					Acidic (4.7)	
A12L	126512	125937	192	20.5	Basic (10.1)	
A13L	126748	126539	70	7.7	Basic (9.7)	
A14L	127128	126859	90	10.0	-	
A15L	127580	127299	94	11.0	-	
A16L	128700	127567	378	43.6	Hydrophobic C-terminus	
A17L	129314	128706	203	23.0	Hydrophobic center	
					Acidic (4.1)	
A18R	129329	130807	493	56.7	Basic (9.3)	

TABLE 1—*Continued*

Gene[a]	Translation Start	Translation Stop[b]	Size aa	Size M_r[c]	Characteristics	References
A19L	131024	130794	77	8.3	-	
A20R	131377	132654	426	49.2	-	
A21L	131378	131028	117	13.6	Hydrophobic N-terminus	
A22R	132620	133147	176	20.7	Basic (9.9)	
A23R	133170	134315	382	44.6	-	
A24R	134315	137806	1164	133.4	RNA polymerase subunit;	Hooda-Dhingra, *et al.* (1990)
					ts: C27, C29, C32, C47, C62	Hooda-Dhingra, *et al*, (1990)
					Leucine Zipper Pattern	
A25L	138011	137817	65	7.5	A-type inclusion protein (cowpox virus)	Funahashi, *et al.* (1988);
					Acidic (3.3)	
A26L	138948	137983	322	37.3	A-type Inclusion protein (cowpox virus)	Funahashi, *et al.* (1988);
					Basic (9.2)	
A27L	139330	139001	110	12.6	Fusion protein	Rodriguez & Esteban (1987)
A28L	139771	139334	146	16.3	-	
A29L	140689	139775	305	35.4	-	
A30L	140885	140655	77	8.7	Basic (9.9)	
A31R	141045	141416	124	14.2	Basic (9.0)	
					Ribonucleoprotein RNA-binding region signature	
A32L	142288	141389	300	34.4	Basic (9.2)	
					ATP/GTP Binding motif A	
A33R	142316	142870	185	20.5	-	
A34R	142897	143400	168	19.5	Basic (10.1)	
A35R	143447	143974	176	20.0	Acidic (4.0)	
A36R	144044	144706	221	25.1	Acidic (4.4)	
A37R	144773	145561	263	29.9	-	
A38L	146678	145848	277	31.6	Multiply hydrophobic	
A39R	146695	147903	403	45.7	-	

A40R	147932	148435	168	19.3	Hydrophobic N-terminus	
A41L	149155	148499	219	25.1	Acidic (4.8)	
A42R	149334	149732	133	15.0	Basic (9.9)	
					Profilin	
A43R	149773	150354	194	22.6	-	
A44L	151733	150696	346	39.4	*3ß-Hydroxy-5-ene steroid dehydrogenase*	
A45R	151780	152154	125	13.8	*Superoxide dismutase*	
A46R	152147	152788	214	24.7	-	
A47L	153690	152959	244	28.3	Basic (10.0)	
A48R	153789	154400	204	23.2	**Thymidylate kinase**	Smith, *et al.* (1989a)
					ATP/GTP binding motif A	
					Acidic (5.0)	
A49R	154451	154936	162	18.8	Acidic (3.9)	
A50R	154972	156627	552	63.4	**DNA Ligase**	Colinas, *et al.* (1990); Smith, *et al.* (1989a); Kerr and Smith (1989)
					Nonessential	Colinas, *et al.* (1990)
A51R	156683	157684	334	37.7	Nonessential	Davis, *et al.* (unpublished)
A52R	157757	158326	190	22.7	Hydrophilic N-terminus	
A53R	158635	158943	103	12.0	Nonessential	Davis, *et al.* (unpublished)
A54L	158743	158474	90	10.8	Basic (10.4)	
					Nonessential	Davis, *et al.* (unpublished)
A55R	159442	161133	564	64.7	Nonessential	Davis, *et al.* (unpublished)
A56R	161186	162130	315	34.8	Nonessential	Shida, *et al.* (1987)
					Hemagglutinin	Shida (1986)
					Hydrophobic C-terminus	
					Acidic (3.9)	
A57R	162278	162730	151	17.4	-	

TABLE 1—*Continued*

Gene[a]	Translation Start	Translation Stop[b]	Size aa	Size M_r[c]	Characteristics	References
B1R	162884	163783	300	34.3	ts: C2, C3, C25 Protein Kinase Basic (9.1)	Traktman, *et al.* (1989a) Howard and Smith (1989)
B2R	163876	164532	219	24.6	-	
B3R	164571	164942	124	14.4	Acidic (4.7)	
B4R	165603	167276	558	65.3	-	
B5R	167383	168333	317	35.1	Multiply hydrophobic Acidic (4.4) *Complement control proteins* *C3L homologue*	
B6R	168432	168950	173	20.1	-	
B7R	168991	169536	182	21.3	Hydrophobic N-terminus	
B8R	169594	170409	272	31.2	Hydrophobic N-terminus	
B9R	170499	170729	77	8.8	-	
B10R	170695	171192	166	18.9	-	
B11R	171267	171530	88	9.9	Acidic (3.6) $M(DT)_9DVTNV...$	
B12R	171600	172448	283	33.4	Protein Kinase	Howard and Smith (1989)
B13R	172562	172909	116	12.8	Hemorrhage-inducing Serine Protease Inhibitor Nonessential Acidic (4.6)	Pickup, *et al.* (1986) Kotwal and Moss (1989); Perkus, *et al.* (1990b)
B14R	172887	173552	222	24.9	Hemorrhage-inducing Serine Protease Inhibitor Nonessential Acidic (4.3)	Pickup, *et al.* (1986) Kotwal and Moss (1989) Perkus, *et al.* (1990b)
B15R	173632	174078	149	17.4	Nonessential Acidic (4.5)	Perkus, *et al.* (1990b)
B16R	174272	175141	290	32.5	Nonessential *Kinase-related transforming protein*	Perkus, *et al.* (1990b)
B17L	176212	175193	340	39.5	Nonessential	Perkus, *et al.* (1990b)
B18R	176349	178070	574	68.1	Nonessential	Perkus, *et al.* (1990b)

B19R	178145	179203	353	40.9	Hydrophobic N-terminus Nonessential	Perkus, *et al.* (1990b)
B20R	179300	179680	127	15.5	Nonessential Acidic (4.1)	Perkus, *et al.* (1990b)
B21R*	180585	180857	91	10.5	Nonessential; C15L	Perkus, *et al.* (1990b)
B22R*	181199	181741	181	21.0	Nonessential; C16L	Perkus, *et al.* (1990b)
B23R*	181791	182948	386	44.9	Nonessential; C17L	Perkus, *et al.* (1990b)
B24R*	183045	183494	150	17.5	Nonessential; C18L Acidic (4.8)	Perkus, *et al.* (1990b)
B25R*	183882	184658	259	30.5	Hydrophobic N-terminus Nonessential; C19L	Perkus, *et al.* (1990b)
B26R*	184606	184914	103	12.5	Nonessential; C20L Basic (9.0)	Perkus, *et al.* (1990b)
B27R*	184923	185261	113	13.4	Nonessential; C21L	Perkus, *et al.* (1990b)
B28R*	185625	185990	122	13.6	Nonessential; C22L Hydrophobic N-terminus	Perkus, *et al.* (1990b)
B29R*	186730	187461	244	26.4	Nonessential; C23L Acidic (4.2)	Perkus, *et al.* (1990b)

[a] Open reading frames enumerated as described in text.

[b] Translation stop does not incude the three bases of termination codon.

[c] M_r values calculated for the nascent, unprocessed polypeptide chain are presented as kDa.

[d] Functions or activities indicated in bold type are known functions of vaccinia virus. Those indicated in *italics* have been identified in this study on the basis of similarity to existing proteins. All others are possible functions previously described by other investigators.

[e] Acidic proteins: p*I* < 5.0; basic proteins: p*I* > 9.0. p*I* presented within parentheses.

[f] Temperature-sensitive mutants indicated by *ts*. Those first isolated by Condit *et al.* (1983) are prefaced with C; t
begin with E. Mutant C19, while not localized to a particular open reading frame, appears to map in the vicinity of I

* Open reading frames repeated in both left and right termini of genome.

Please **REPLACE** References, pages 26-28, in the specification as follows:

REFERENCES

AHN, B.-Y., JONES, E. V., and MOSS, B. (1990). Identification of the vaccinia virus gene encoding an 18-kilodalton subunit of RNA polymerase and demonstration of a 5' poly(A) leader on its early transcript. *J. Virol.* 64, 3019–3024.

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Please **REPLACE** Table 2, pages 29-45 in the specification, as follows:

TABLE 2

Features and Homologies of Open Reading Frames of the Vaccinia MVA Strain

ORF[a]	START STOP	AA[b]	kDa[c]	name / (putative) function / homologies[g]	BLAST[d] expect	BLAST[e] AA Id	HSS[f] (%)	references
left terminal region:								
001L/ 193R[h]	6822 6412	136	14.9	35k major secr. protein chemokine receptor (f[i])				(Patel *et al.*, 1990) (Graham *et al.*, 1997)
C23L		244		VAC (*C23L/B29R*)	6.0e-57	41/42	97	(Goebel *et al.*, 1990)
		253		VAR-I[j] G3R	8.9e-51	46/49	93	(Shchelkunov *et al.*, 1995)
		246		CPX ORF B	5.6e-49	40/42	95	(Hu *et al.*, 1994)
		258		SFV T1 protein	2.5e-20	23/42	54	(Upton *et al.*, 1987)
		260		Myxoma virus T1/35kDa	1.5e-14	21/42	50	(Graham *et al.*, 1997)
002L/ 192R[h]	7784 7254	176	19.7	secr. TNF receptor (f)				(Upton *et al.*, 1991a)
		355		CPX crmB	5.1e-71	76/83	91	(Hu *et al.*, 1994)
		348		VAR-BSH G2R	1.0e-66	73/83	87	(Shchelkunov *et al.*, 1995)
		326		Myxoma virus T2	4.9e-30	21/37	56	(Upton *et al.*, 1991a)
		325		Rabbit fibroma Virus T2	1.8e-28	17/36	47	(Upton *et al.*, 1987)
		202		CPX C4L	8.7e-15	30/51	58	(Safronov *et al.*, 1996)
		346		HS TNF receptor protein	1.9e-08	14/26	53	(Heller *et al.*, 1990)
C19L		259		VAC (*C19L/B25R*)	0.00026	16/19	84	(Goebel *et al.*, 1990)
		277		human CD40L receptor	0.0015	11/24	45	(Stamencovic *et al.*, 1989)
				30 matches to TNF receptors and surface proteins	<0.39			
003L/ 191R[h]	8780 8472	102	12.1	45k ank[k]-like protein (f1)				(Goebel *et al.*, 1990)
C17L		386		VAC C17L/B23R	1.3e-39	62/63	98	(Goebel *et al.*, 1990)
004L/ 190R[h]	9558 8857	233	26.9	45k ank-like protein (f2)				(Goebel *et al.*, 1990)
C17L		386		VAC (C17L/B23R)	6.2e-159	110/110	100	(Goebel *et al.*, 1990)
D1L		91		VAR-BSH	9.1e-31	46/49	93	(Shchelkunov *et al.*, 1995)
		669		CPX host range	1.1e-13	22/50	44	(Spehner *et al.*, 1988)
		452		VAR-I D6L (BSH:D8L)	1.7e-11	21/50	42	(Shchelkunov *et al.*, 1995)
		574		VAR-I B19R (BSH: B16R)	1.2e-05	22/73	30	(Shchelkunov *et al.*, 1995)
		574		VAC B18R (WR: B17R)	8.6e-05	22/73	30	(Goebel *et al.*, 1990)
		634		VAC C9L	0.00011	11/24	45	(Kotwal and Moss, 1988a)
		585		VAR-I G1R	0.00013	22/74	29	(Shchelkunov *et al.*, 1995)
		516		orf virus	0.0088	15/49	30	(Sullivan *et al.*, 1995b)
		153		VAR-I D7L (BSH:D10L)	0.014	12/28	42	(Shchelkunov *et al.*, 1995)
005R	10203 10625	140	15.5	Growth factor (EGF receptor binding)				(Twardzik *et al.*, 1985) (Stroobant *et al.*, 1985)
C11R		142		VAC	2.9e-82	99/104	95	(Goebel *et al.*, 1990)
D2R		140		VAR-I (BSH:D4R)	3.6e-74	106/140	75	(Shchelkunov *et al.*, 1995)
		138		CPX D5R	3.4e-95	101/114	88	(Safronov *et al.*, 1996)
		169		human epiregulin	2.2e-14	29/78	37	D30783
				100 matches to growth factor like sequences	<0.10			

006L	11758	326	37.9	**37.9k protein**				(Venkatesan *et al.*, 1982)
C10L	10778	331		VAC	1.7e-235	264/268	98	(Goebel *et al.*, 1990)
		331		CPX D6L	7.7e-235	264/268	98	(Safronov *et al.*, 1996)
D5L		330		VAR-BSH (I: D3L)	3.6e-233	169/171	97	(Shchelkunov *et al.*, 1995)
		316		VAR-I D11L (BSH:D14L)	1.7e-94	34/68	44	(Shchelkunov *et al.*, 1995)
		316		VAC C4L	1.8e-92	30/68	54	(Goebel *et al.*, 1990)
		315		CPX D16L	2.3e-92	31/68	45	(Safronov *et al.*, 1996)
		82		Ectromelia 42K protein	1.2e-50	78/82	95	(Senkevich *et al.*, 1993a)
		418		FPV BamHI ORF1	3.0e-11	13/41	31	(Tomley *et al.*, 1988)
007R	12263	91	10.6	**28k virulence factor (f)**				(Senkevich *et al.*, 1993a)
	12538	242		CPX D7R	1.5e-51	42/47	89	(Safronov *et al.*, 1996)
		184		VAC-WR 21.7k protein	5.3e-51	41/47	87	(Kotwal and Moss, 1988a)
D4R		242		VAR-I (BSH:D6R)	3.7e-50	41/47	87	(Shchelkunov *et al.*, 1995)
		241		Ectromelia 28k secreted virulence factor	3.7e-50	41/47	87	(Senkevich *et al.*, 1993a)
008L	13414	120	13.7	**13.7k protein**				
D7L	13052	126		VAR-BSH (I:D5L)	1.9e-83	57/64	89	(Shchelkunov *et al.*, 1995)
		138		Ectromelia 16k protein	7.8e-81	58/60	96	(Senkevich *et al.*, 1993a)
		124		CPX D8L	3.2e-67	49/60	81	(Safronov *et al.*, 1996)
		68		7.8k protein (VAC-WR)	1.3e-34	53/64	82	(Kotwal and Moss, 1988a)
009L	13745	90	10.7	**77k CPX hr protein (f1)**				(Spehner *et al.*, 1988)
	13473	669		CPX host range gene	2.7e-46	43/52	82	(Safronov *et al.*, 1996)
		634		VAC C9L	1.7e-05	9/33	27	(Goebel *et al.*, 1990)
010L	14186	142	16.1	**77k CPX hr protein (f2)**				(Spehner *et al.*, 1988)
	13758	669		CPX host range gene	2.2e-91	133/142	93	(Safronov *et al.*, 1996)
		634		VAC C9L	9.2e-21	26/63	41	(Goebel *et al.*, 1990)
D6L		452		VAR-I (BSH: D8L)	4.5e-13	27/29	93	(Shchelkunov *et al.*, 1995)
		150		VAC C18L/B24R	1.3e-11	19/52	36	(Goebel *et al.*, 1990)
		439		AT ankyrin repeat protein	9.5e-07	23/59	38	(Zhang *et al.*, 1992)
		558		VAR-I B6R (BSH:B5R)	4.0e-05	28/113	24	(Shchelkunov *et al.*, 1995)
				30 matches with ankyrin repeat containing proteins	2.7e-05 to 0.016			
011L	14682	135	15.8	**77k CPX hr protein (f3)**				(Spehner *et al.*, 1988)
	14275	669		CPX host range gene	7.6e-80	54/64	84	(Safronov *et al.*, 1996)
D6L		452		VAR-I (BSH: D8L)	9.2e-78	52/64	81	(Shchelkunov *et al.*, 1995)
012L	15183	90	10.3	**77k CPX hr protein (f4)**				(Spehner *et al.*, 1988)

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GENOMIC SEQUENCE OF THE MVA STRAIN

ORF[a]	START STOP	AA[b]	kDa[c]	name / (putative) function / homologies[g]	BLAST[d] expect	BLAST[e] AA id	HSS[f] (%)	references
left terminal region:								
D6L	14911	452		VAR-I (BSH: D8L)	2.2e-52	80/85	94	(Shchelkunov *et al.*, 1995)
		669		CPX host range gene	8.1e-51	77/85	90	(Spehner *et al.*, 1988)
		153		VAR-I D7L (BSH: D10L)	2.9e-17	19/45	42	(Shchelkunov *et al.*, 1995)
		634		VAC C9L	1.3e-13	19/45	42	(Goebel *et al.*, 1990)
		1161		C. botulinum NTNH protein	0.00019	6/12	50	(Hutson *et al.*, 1996)
		202		Capripox	0.00058	15/58	25	(Cao *et al.*, 1995)
		895		UDP glucose dehydrogenase	0.00051	6/19	31	(Bult *et al.*, 1996)
		516		orf virus ank-like	0.0064	16/49	32	(Sullivan *et al.*, 1995b)
		673		rabbit fibroma 77.2k protein	0.0072	12/30	40	(Massung *et al.*, 1992)
013L	15420	71	8.5	**77k CPX hr protein (f5)**				(Spehner *et al.*, 1988)
	15205	669		CPX host range gene	5.2e-44	68/69	98	(Safronov *et al.*, 1996)
D6L		452		VAR (BSH: D8L)	7.9e-42	64/67	95	(Shchelkunov *et al.*, 1995)
		673		rabbit fibroma 77.2k protein	0.0052	8/26	30	(Massung *et al.*, 1992)
		386		VAC C17L/B23R	0.018	14/33	42	(Goebel *et al.*, 1990)
		202		Capripox	0.023	10/19	52	(Sullivan *et al.*, 1995b)
		574		VAC B18R (WR: B17R)	0.71	12/28	42	(Goebel *et al.*, 1990)
		574		VAR B19R (BSH:B16R)	0.71	12/28	42	(Shchelkunov *et al.*, 1995)
014L	16205	109	13.1	**75k ank-like gene (f1)**				(Kotwal and Moss, 1988a)
C9L	15876	634		VAC	3.9e-73	109/109	100	(Goebel *et al.*, 1990)
		614		CPX D11L	1.6e-70	105/108	97	(Safronov *et al.*, 1996)
D9L		91		VAR (I: D6.5L)	1.2e-52	78/91	85	(Shchelkunov *et al.*, 1995)
		437		CPX D1L	3.7e-19	28/67	41	(Safronov *et al.*, 1996)
		673		rabbit fibroma 77.2K protein	0.021	5/16	31	(Massung *et al.*, 1992)
015L	16786	96	11.2	**75k ank-like gene (f2)**				(Kotwal and Moss, 1988a)
C9L	16496	634		VAC	4.0e-53	80/80	100	(Goebel *et al.*, 1990)
		614		CPX D11L	3.9e-25	48/80	60	(Safronov *et al.*, 1996)
		437		CPX D1L	9.6e-12	14/36	38	(Safronov *et al.*, 1996)
		172		VAR-Garcia 1966 B11L	0.0001	17/17	100	(Massung *et al.*, 1996)
		141		integrase (simian foamy v.)	0.033	10/24	41	(Schweizer and Neumann, 1995)
		669		CPX host range gene	0.043	9/17	52	(Spehner *et al.*, 1988)
016L	17759	297	35.0	**75k ank-like gene (f3)**				(Kotwal and Moss, 1988a)
C9L	16866	634		VAC	3.4e-208	291/294	98	(Goebel *et al.*, 1990)
		614		CPX D11L	1.4e-130	90/126	71	(Safronov *et al.*, 1996)
D7L		153		VAR-I (BSH:D10L)	8.4e-68	84/109	77	(Shchelkunov *et al.*, 1995)
		669		CPX host range gene	4.5e-17	24/61	39	(Spehner *et al.*, 1988)
		452		CPX D9L	2,2e-16	23/61	37	(Safronov *et al.*, 1996)
D8L		668		VAR-BSH (I:D6L)	3.3e-16	21/61	34	(Shchelkunov *et al.*, 1995)
		386		VAC C17L/B23R	2.9e-08	11/24	45	(Goebel *et al.*, 1990)
		833		CPX D3L	0.0085	13/58	22	(Safronov *et al.*, 1996)
		574		VAC B18R (WR:B17R)	0.012	13/40	32	(Goebel *et al.*, 1990)
		202		Capripox virus	0.084	11/29	37	(Sullivan *et al.*, 1995b)
		574		VAR-I B19R (BSH:B16R)	0.090	13/40	32	(Shchelkunov *et al.*, 1995)

017L	18335	177	20.8	**20.8k protein**				(Kotwal and Moss, 1988a)
C8L	17802	184		VAC	1.2e-125	125/129	96	(Goebel *et al.*, 1990)
		182		CPX D12L	5.0e-118	119/126	94	(Safronov *et al.*, 1996)
		182		VAC B7R	8.3e-06	16/67	23	(Goebel *et al.*, 1990)
		795		VAC H4L (RAP94)	0.60	12/45	26	(Goebel *et al.*, 1990)
018L	18859	150	18.0	**host range protein**				(Perkus *et al.*, 1991)
C7L	18407	150		VAC	1.6e-106	150/150	100	(Kotwal and Moss, 1988a)
D11L		150		VAR-BSH (I:D8L)	4.2e-106	149/150	99	(Shchelkunov *et al.*, 1995)
		185		Swinepox virus ORF SwF8a	3.4e-35	31/82	37	(Schnitzlein and Tripathy, 1991)
		197		Capripox virus ORF CF8a	1.4e-31	29/87	33	(Gershon and Black, 1989a)
		170		CPX D4L	3.5e-17	19/60	31	(Safronov *et al.*, 1996)
		158		Myxoma virus ORF MF8	5.6e-13	16/43	37	(Jackson and Bults, 1992)
		128		VAR-BSH D3L (I:D1.5L)	5.4e-06	18/60	30	(Shchelkunov *et al.*, 1995)
019L	19541	157	18.2	**18.2k protein**				(Kotwal and Moss, 1988a)
C6L	19068	151		VAC	7.6e-104	151/151	100	(Goebel *et al.*, 1990)
D9L		156		VAR (BSH: D12L)	1.6e-99	145/150	96	(Shchelkunov *et al.*, 1995)
		156		CPX D14L	1.3e-96	141/150	94	(Safronov *et al.*, 1996)
		159		Capripox virus ORF T3a	4.4e-07	24/76	31	(Gershon and Black, 1989a)
		151		Rabbit fibroma virus T3Aa	0.0047	16/46	34	(Upton *et al.*, 1987)
		181		VAC C16L/B22R	0.2	12/46	26	(Goebel *et al.*, 1990)
		149		VAR C4R	0.29	8/13	61	(Shchelkunov *et al.*, 1995)
		149		VAC-WR K7R	0.40	8/13	61	(Kotwal and Moss, 1988a)
020L	20025	113	13.2	**14k virulence factor,**				(Kotwal and Moss, 1988a)
	19684			**secreted protein (f)**				(Kotwal and Moss, 1988b)
N1L		117		VAC	2.6e-60	92/102	90	(Goebel *et al.*, 1990)
		117		CPX P1L	7.3e-58	85/102	83	(Shchelkunov *et al.*, 1995)
P1L		117		VAR-BSH, virokine	6.6e-56	88/102	86	(Safronov *et al.*, 1996)
		107		Rabbit fibroma virus	0.015	10/17	58	(Massung *et al.*, 1992)
021L	20656	170	20.3	**alpha-amanitin sensitive**				(Tamin *et al.*, 1991)
	20144			**protein**				(Kotwal and Moss, 1988a)
		175		CPX P2L	3.0e-118	138/142	97	(Safronov *et al.*, 1996)
N2L		175		VAC	6.1e-118	137/142	96	(Goebel *et al.*, 1990)
P2L		177		VAR	9.7e-115	135/142	95	(Shchelkunov *et al.*, 1995)
022L	20981	98	11.0	**33k host range gene (f)**				(Gillard *et al.*, 1986)
K1L	20685	284		VAC	1.8e-56	86/88	97	(Altenburger *et al.*, 1989)
		284		CPX M1L	2.3e-56	86/88	97	(Safronov *et al.*, 1996)
C1L		66		VAR	2.0e-39	63/66	95	(Shchelkunov *et al.*, 1995)
		65		human NOTCH 2	0.00036	17/41	41	(Katsanis *et al.*, 1996)

ORF[a]	START STOP	AA[b]	kDa[c]	name / (putative) function / homologies[g]	BLAST[d] expect	BLAST[e] AA id	HSS[f] (%)	references
left terminal region:								
023L	22296 21187	369	42.3	serpin SPI-3, cell-cell fusion mutation				(Boursnell *et al.*, 1988) (Altenburger *et al.*, 1989)
K2L		369		VAC	1.2e-258	365/369	98	(Goebel *et al.*, 1990)]
C2L		373		CPX M2L	1.2e-256	331/337		(Safronov *et al.*, 1996)
		373		VAR-BSH	9.9e-249	321/337	95	(Shchelkunov *et al.*, 1995)
		373		Ectromelia virus H14-B	6.5e-244	312/337		U67964
		386		HS plasminogen activator inhibitor 1	1.1e-35	30/68	44	(Loskutoff *et al.*, 1987)
		58		CPX SPI 3 protein	8.2e-33	57/58	98	gi:1168082
		369		Myxoma virus MAP1 gene	7.3e-32	33/131	25	(Upton *et al.*, 1990a)
		397		mouse protease nexin	1.5e-29	31/67	46	(Vassalli *et al.*, 1993)
		397		humane glia derived neurite-promoting factor	8.7e-27	30/65	46	A03911
		320		Swinepox SPI like protein	3.6e-21	20/70	28	(Massung *et al.*, 1993)
		417		a-1 antitrypsin, human	2.2e-20	26/66	39	(Ciliberto *et al.*, 1985)
		383		Corticosteroid-binding protein (rabbit)	9.0e-20			(Seralini *et al.*, 1989)
		390		squamous cell carcinoma antigen	1.9e-17			(Schneider *et al.*, 1995)
024L	22612 22346	88	10.5	IFN resistance, eIF-2a homolog				(Beattie *et al.*, 1991) (Davies *et al.*, 1992)
		88		CPX M3L	2.6e-61	88/88	100	(Safronov *et al.*, 1996)
K3L		88		VAC	1.4e-60	87/88	98	(Goebel *et al.*, 1990)
C3L		88		VAR-I	1.0e-52	73/88	82	(Shchelkunov *et al.*, 1995)
		86		SPV C8 protein	4.1e-22	20/44	45	(Massung *et al.*, 1993)
				translation initiation factor 2 family	1.2e-08/ 0.45			
025L	23938 22664	424	48.9	phospholipase D-like protein				(Cao *et al.*, 1997)
K4L		424		VAC	1.5e-306	423/424	99	(Goebel *et al.*, 1990)
		424		CPX M4L	2.1e-303	416/424	98	(Safronov *et al.*, 1996)
		437		human HU-K4	2.8e-135	53/95	55	U60644
		372		D. discoideum	2.5e-91	28/47	59	(Giorda *et al.*, 1989)
		516		C. elegans	6.6e-89	31/61	50	gi: 2435624
		2327		C. elegans	2.8e-52	36/60	60	gi: 2291241
		635		C. elegans	1.1e-24	19/53	35	(Wilson *et al.*, 1994)
		377		FPV major envelope protein	2.9e-23	19/61	31	(Calvert *et al.*, 1992)
		371		Myxoma virus env protein	3.6e-22	18/51	35	U43549
		378		Orf virus env protein B2L	1.2e-21	21/71	29	(Sullivan *et al.*, 1994)
MC021L		388		MCV subtype 1 env protein	3.2e-21	20/63	31	(Senkevich *et al.*, 1997)
C17L		372		VAR-BSH	4.6e-19	15/52	28	(Shchelkunov *et al.*, 1995)
		372		VAC F13L	4.9e-17	15/52	28	(Goebel *et al.*, 1990)

026L	24478	170	19.1	lysophospholipase-like protein (f1)				(Upton & Buller, unpub.)
	23966							
		276		CPX M5L	2.6e-110	161/170	94	(Safronov *et al.*, 1996)
		277		Ectromelia virus H14-E	2.7e-109	160/170	94	X94355 U67964
K5L		136		VAC	5.5e-69	107/108	99	(Goebel *et al.*, 1990)
		134		VAC-WR	8.3e-63	98/101	97	(Boursnell *et al.*, 1988)
		313		HS lysophospholipase	3.3e-35	35/105	33	U67963
		323		homolog	1.2e-13	30/94	31	Z97050
		324		poss. oxidoreductase M. tuberculosum	3.1e-5	13/58	22	U95973
		313		Lysophospholipase isolog A. thaliana	0.047	13/30	43	U32747
				H. influenza probable lysophospholipase L2				
027L	24694	64	7.0	lysophospholipase-like protein (f2)				(Upton & Buller, unpub.)
	24500							
K6L		81		VAC	5.3e-42	63/63	100	(Boursnell *et al.*, 1988)
		276		CPX M5L	2.4e-36	57/58	98	(Safronov *et al.*, 1996)
		277		Ectromelia virus H14-E	2.4e-36	57/58	98	U67964
		313		HS lyophospholipase homolog	9.1e-23	34/53	64	U67963
		323		hyp. oxidoreductase M. tuberculosis	9.9e-14	22/54	40	Z97050
		530		dihydrotestosterone/androstanediol UDP-glucuronosyl-transferase	7.0e-05	6/17	35	A48633

central conserved region:								
028R	24864	149	17.5	17.5k protein				(Goebel *et al.*, 1990)
K7R	25313	149		VAC	6.1e-105	149/149	100	(Goebel *et al.*, 1990)
		161		CPX M6R	1.6e-101	144/149	96	(Safronov *et al.*, 1996)
C4R		149		VAR	4.9e-101	143/149	100	(Shchelkunov *et al.*, 1995)
		236		Swinepox (sc76)	0.00017	19/49	95	(Massung *et al.*, 1993)
029L	26046	222	25.9	25.9k protein				(Roseman and Slabaugh, 1990)
F1L	25378	226		VAC	2.7e-158	208/211	98	(Goebel *et al.*, 1990)
		238		CPX G1L	7.0e-148	166/189	87	(Safronov *et al.*, 1996)
C5L		251		VAR-I	6.6e-147	184/200	92	(Shchelkunov *et al.*, 1995)
030L	26501	147	16.2	dUTPase				(Roseman and Slabaugh, 1990)
	26058							(Roseman *et al.*, 1996)
F2L		147		VAC	2.9e-102	147/147	100	(Goebel *et al.*, 1990)
		147		CPX G2L	8.2e-100	144/147	97	(Safronov *et al.*, 1996)
C6L		147		VAR	1.1e-97	142/147	96	(Shchelkunov *et al.*, 1995)
		164		human dUTPase	4.1e-61	49/69	71	(Ladner *et al.*, 1996)

GENOMIC SEQUENCE OF THE MVA STRAIN

ORF[a]	START STOP	AA[b]	kDa[c]	name / (putative) function / homologies[g]	BLAST[d] expect	BLAST[e] AA id	HSS[f] (%)	references
left terminal region:								
		142		Swinepox virus	8.0e-56	43/70	61	(Massung *et al.*, 1993)
		159		orf virus	1.5e-49	45/69	65	(Mercer *et al.*, 1989)
		178		avian adenovirus	6.6e-49	40/70	57	(Akopian *et al.*, 1992)
		1124		FIV pol polyprotein	1.5e-26	49/117	41	(Talbott *et al.*, 1989)
				dUTPase pyrophosphatase family	>4.2e-06			
031L	27955 26525	476	55.3	**kelch-like protein**				(Senkevich *et al.*, 1993b) (Roseman and Slabaugh, 1990)
F3L		480		VAC	0.0	292/294	99	(Goebel *et al.*, 1990)
		485		CPX G3L	0.0	287/293	97	(Safronov *et al.*, 1996)
C7L		179		VAR-1	1.9e-124	166/179	92	(Shchelkunov *et al.*, 1995)
		500		Swinepox virus protein C13	4.4e-46	39/133	29	(Massung *et al.*, 1993)
		564		VAC A55R	2.8e-21	17/51	33	(Goebel *et al.*, 1990)
		689		kelch protein D.melanogaster	5.3e-18	21/65	32	(Xue and Cooley, 1993)
		512		CPX D18L	1.4e-16	15/33	45	(Safronov *et al.*, 1996)
		512		VAC C2L	1.6e-16	15/33	45	(Goebel *et al.*, 1990)
		625		T27E9.4 C. elegans	3.7e-14	15/59	25	Z82059
		624		human KIAA0132 protein	1.9e-13	13/60	21	D50922 o.k
		817		R09A8.3 (C. elegans)	1.1e-12	17/45	37	(Wilson *et al.*, 1994)
		611		C47D12.7 (C. elegans)	2.4e-12	22/91	24	(Wilson *et al.*, 1994)
		530		Swinepox virus	3.0e-09	14/58	24	(Massung *et al.*, 1993)
		589		MM[m] actin binding protein	1.9e-09	18/88	20	U65079
		521		CPX C3L	1.2e-08	15/37	40	(Safronov *et al.*, 1996)
		509		Myxoma virus MT-9	2.5e-08	17/58	29	(Upton *et al.*, 1990a)
		202		Murine IAP-promoted placenta (MIPP) expressed	4.3e-08	17/56	30	(Chang-Yeh *et al.*, 1991)
		326		protein	3.9e-06	22/80	27	Z99708
		559		A. thaliana hyp. protein	9.0e-6	12/31	38	(Senkevich *et al.*, 1993b)
		916		Ectromelia virus p65	0.00016	13/42	30	(Way *et al.*, 1995)
		172		ß-scruin (L. polyphemus)	0.018	15/36	41	(Shchelkunov *et al.*, 1995)
				VAR-I J8R (BSH: J6R)				
032L	28925 27966	319	37.0	**ribonucleotide reductase (small subunit)**				(Slabaugh *et al.*, 1988) (Roseman and Slabaugh, 1990)
		319		CPX G4L	2.3e-231	317/319	99	(Safronov *et al.*, 1996)
F4L		319		VAC	3.5e-231	317/319	99	(Goebel *et al.*, 1990)
C8L		333		VAR-BSH	4.1e-228	313/319	98	(Shchelkunov *et al.*, 1995)
				ribonucleotide reductase family	>2.2e-10			

033L	29250	97	11.1	36.5k major membrane				(Roseman and Slabaugh, 1990)
	28957			protein precursor (f1)				
C9L		348		VAR-BSH	1.9e-36	51/53	96	(Shchelkunov *et al.*, 1995)
		323		CPXG5L	2.4e-19	47/77	61	(Safronov *et al.*, 1996)
F5L		321		VAC	3.3e-19	42/70	60	(Goebel *et al.*, 1990)
		1584		non-receptor tyrosin kinase (Dictyostelium discoideum)	0.00038	15/35	42	(Tan and Spudich, 1990)
034L	29875	218	24.8	36.5k major membrane				(Roseman and Slabaugh, 1990)
	29219			protein precursor (f2)				
		323		CPXG5L	8.2e-155	215/217	99	(Safronov *et al.*, 1996)
F5L		321		VAC	6.4e-155	215/217	99	(Goebel *et al.*, 1990)
C9L		348		VAR-BSH	6.8e-141	186/210	88	(Shchelkunov *et al.*, 1995)
035L	30129	74	8.6	8.6k protein				(Roseman and Slabaugh, 1990)
F6L	29905	74		VAC	5.5e-47	74/74	100	(Goebel *et al.*, 1990)
C10L		72		VAR	2.3e-38	62/70	88	(Shchelkunov *et al.*, 1995)
036L	30387	80	9.4	9.4k protein				(Roseman and Slabaugh, 1990)
C11L	30145	79		VAR	2.9e-44	34/43	79	(Shchelkunov *et al.*, 1995)
F7L		92		VAC	1.9e-43	65/65	100	(Goebel *et al.*, 1990)
037L	30731	65	7.9	7.9k protein				(Roseman and Slabaugh, 1990)
F8L	30534	65		VAC	5.1e-43	63/65	96	(Goebel *et al.*, 1990),
C12L		65		VAR-I	3.1e-41	61/65	93	(Shchelkunov *et al.*, 1995)
038L	31429	212	23.8	23.8k protein				(Roseman and Slabaugh, 1990)
F9L	30791	212		VAC	7.1e-148	212/212	100	(Goebel *et al.*, 1990),
C13L		212		VAR	1.2e-144	207/212	97	(Shchelkunov *et al.*, 1995)
		215		Swinepox virus	8.1e-72	39/93	41	(Massung *et al.*, 1993)
MC016L		213		MCV subtype 1	2.8e-62	71/152	46	(Senkevich *et al.*, 1996)
		225		Orf virus	5.1e-39	27/84	32	(Mercer *et al.*, 1995)
		243		FPV protein FP2	2.8e-17	26/58	44	(Binns *et al.*, 1988)
		243		MCV subtype 1 MC069R	7.7e-12	23/58	39	(Senkevich *et al.*, 1996)
		250		VAC LIR	1.1e-07	20/58	34	(Goebel *et al.*, 1990),
		250		VAR MIR	1.1e-07	20/58	34	(Shchelkunov *et al.*, 1995)
039L	32735	439	52.1	serine/threonine protein				(Lin and Broyles, 1994)
	31416			kinase 2				(Wang and Shuman, 1995)
F10L		439		VAC	0.0	429/439	97	(Goebel *et al.*, 1990),
C14L		439		VAR-BSH	0.0	424/439	96	(Shchelkunov *et al.*, 1995)
		440		Swinepox virus	2.2e-233	151/214	70	(Massung *et al.*, 1993)
MC017L		443		MCV subtype 1	2.3e-198	178/282	63	(Senkevich *et al.*, 1996)
		498		orf virus	2.2e-162	198/366	54	(Mercer *et al.*, 1995)
040L	33012	84	9.6	39.7k protein (f1)				
C15L	32758	354		VAR	6.6e-27	50/64	78	(Shchelkunov *et al.*, 1995)
F11L		354		VAC	9.1e-27	50/64	78	(Goebel *et al.*, 1990)
041L	33771	100	11.4	39.7k protein (f2)				

ORF[a]	START STOP	AA[b]	kDa[c]	name / (putative) function / homologies[e]	BLAST[d] expect	BLAST[e] AA Id	HSS[f] (%)	references
left terminal region:								
F11L	33469	354		VAC	3.8e-62	95/95	100	(Goebel *et al.*, 1990),
C15L		354		VAR	8.8e-58	90/95	94	(Shchelkunov *et al.*, 1995)
042L	35721	635	73.1	73.1k protein				
F12L	33814	635		VAC	0.0	629/635	99	(Goebel *et al.*, 1990),
C16L		635		VAR-I	0.0	607/635	95	(Shchelkunov *et al.*, 1995)
		352		Myxoma virus	3.6e-84	28/66	42	U43549
MC019L		663		MCV subtype 1	4.0e-60	29/82	35	(Senkevich *et al.*, 1996)
		640		orf virus	4.8e-39	19/61	31	U34774
		630		FPV F12 homolog	2.3e-15	19/67	28	(Ogawa *et al.*, 1993)
043L	36866 35748	372	41.8	37k major EEV antigen IMCBH sensitive protein palmitylprotein				(Hirt *et al.*, 1986) (Schmutz *et al.*, 1991) (Grosenbach *et al.*, 1997)
F13L		372		VAC	2.1e-268	369/372	99	(Goebel *et al.*, 1990)
C17L		372		VAR-BSH	8.9e-265	364/372	97	(Shchelkunov *et al.*, 1995)
		371		Myxoma virus	2.5e-115	110/200	55	U43549
		378		orf virus	7.6e-108	83/194	42	(Sullivan *et al.*, 1994)
MC021L		388		MCV subtype 1	6.1e-98	44/113	38	(Senkevich *et al.*, 1996)
		377		FPV major env protein	2.8e-88	47/112	41	(Calvert *et al.*, 1992)
		251		pigeonpox virus	1.8e-62	47/112	41	S27933
		424		CPX M4L	2.1e-18	16/52	30	(Safronov *et al.*, 1996)
		424		VAC K4L	1.7e-17	14/35	40	(Goebel *et al.*, 1990)
		372		D. discoideum	1.4e-16	28/84	33	(Giorda *et al.*, 1989)
		437		HU-K4 (homo sapiens)	1.5e-11	25/94	26	U60644
044L	37105	73	8.3	8.3k protein				
F14L	36884	73		VAC	2.3e-44	72/73	98	(Goebel *et al.*, 1990)
C18L		73		VAR	2.1e-35	57/73	78	(Shchelkunov *et al.*, 1995)
045L	378533	158	18.6	18.6k protein				
F15L	37377	158		VAC	2.3e-112	157/158	99	(Goebel *et al.*, 1990),
C19L		161		VAR	1.4e-107	150/153	98	(Shchelkunov *et al.*, 1995)
MC025L		148		MCV subtype 1	3.5e-54	52/113	46	(Senkevich *et al.*, 1996)
		148		Myxoma virus	5.4e-50	48/112	42	U43549
046L	38555	231	26.5	26.5k protein				
F16L	37860	231		VAC	3.3e-159	227/231	98	(Goebel *et al.*, 1990),
C20L		231		VAR	5.6e-157	222/231	96	(Shchelkunov *et al.*, 1995)
		209		Myxoma virus	8.3e-48	26/58	44	U43549
MC029L		230		MCV subtype 1	6.9e-45	16/61	26	(Senkevich *et al.*, 1996)
047R	38619 38924	101	11.3	11k DNA binding phosphoprotein				(Bertholet *et al.*, 1985) (Kao and Bauer, 1987)
F17R		101		VAC	3.0e-69	100/101	99	(Goebel *et al.*, 1990)
C21R		101		VAR	9.7e-67	99/101	98	(Shchelkunov *et al.*, 1995)
		102		MYX	6.6e-26	45/92	98	U43549
MC030R		92		MCV subtype 1	1.5e-20	33/53	48	(Senkevich *et al.*, 1997)
		46		orf virus	1.3e-06	16/29	62	(Mercer *et al.*, 1995)

048L	40360	479	55.6	**poly(A) polymerase**				(Gershon *et al.*, 1991)
	38921			**catalytic subunit**				
E1L		479		VAC	0.0	478/479	99	(Goebel *et al.*, 1990),
E1L		479		VAR-I	0.0	472/479	98	(Shchelkunov *et al.*, 1995)
MC031L		470		MCV subtype 1	1.5e-177	114/173	65	(Senkevich *et al.*, 1997)
049L	42570	737	85.9	**85.9k protein**				(Ahn *et al.*, 1990a)
E2L	40357	737		VAC	0.0	735/737	99	(Goebel *et al.*, 1990),
E2L		737		VAR-I	0.0	731/737	99	(Shchelkunov *et al.*, 1995)
MC032L		748		MCV subtype 1	8.3e-127	59/198	29	(Senkevich *et al.*, 1997)
050L	43269	190	21.5	**dsRNA dependent PK**				(Chang *et al.*, 1992)
	42697			**inhibitor, host range**				(Chang *et al.*, 1995b)
E3L		190		VAC	1.4e-129	188/190	98	(Goebel *et al.*, 1990),
E3L		192		VAR-BSH	8.6e-126	111/114	97	(Shchelkunov *et al.*, 1995)
		1175		dsRNA specific ADA (rat)	7.2e-12	22/47	46	(O'Connell *et al.*, 1995)
		1226		dsRNA specific ADA (human)	2.8e-09	21/47	44	(Kim *et al.*, 1994)
		551		human protein kinase p68	3.8e-05	22/42	52	(Meurs *et al.*, 1990)
				INF inducible kinase family	>0.00099			
051L	44103	259	29.8	**RNA polymerase subunit**				(Ahn *et al.*, 1990a)
	43324			**rpo30, VITF-1**				(Broyles and Pennington, 1990)
E4L		259		VAC	1.6e-182	258/259	99	(Goebel *et al.*, 1990)
E4L		259		VAR-BSH	3.2e-180	255/259	98	(Shchelkunov *et al.*, 1995)
MC034L		444		MCV subtype 1	1.2e-84	107/171	62	(Senkevich *et al.*, 1996)
		39		orf virus	6.7e-10	21/39	53	(Mercer *et al.*, 1995)
		243		African swine fever virus	0.00034	17/36	47	(Vydelingum *et al.*, 1993)
				TFIIS family	<0.0096			
052R	44180	331	39.1	**39.1k protein**				(Goebel *et al.*, 1990)
E5R	45175	331		VAC	1.2e-235	329/331	99	(Goebel *et al.*, 1990)
E5R		341		VAR	3.1e-223	312/331	94	(Shchelkunov *et al.*, 1995)
		332		Taterapox	7.1e-225	300/314	95	(Douglas and Dumbell, 1996)
		329		Camelpox	1.4e-221	206/220	93	(Douglas and Dumbell, 1996)
		319		Cowpox	1.5e-202	271/303	89	(Douglas and Dumbell, 1996)
		256		Ectromelia	3.8e-153	218/245	88	(Douglas and Dumbell, 1996)
MC038R		276		MCV subtype 1	8.3e-109	94/152	61	(Senkevich *et al.*, 1997)
053R	45312	567	66.7	**66.7k protein**				(Goebel *et al.*, 1990)

GENOMIC SEQUENCE OF THE MVA STRAIN

ORF[a]	START STOP	AA[b]	kDa[c]	name / (putative) function / homologies[g]	BLAST[d] expect	BLAST[e] AA id	HSS[f] (%)	references
left terminal region:								
E6R		567		VAR	0.0	555/567	97	(Shchelkunov *et al.*, 1995)
MC037R		565		MCV subtype 1	7.2e-247	258/451	57	(Senkevich *et al.*, 1997)
054R	47082	166	19.5	**17k myristylprotein**				(Martin *et al.*, 1997)
E7R	47582	166		VAC	9.7e-116	166/166	100	(Goebel *et al.*, 1990)
E7R		60		VAR-I (BSH: E6.5R)	2.7e-36	53/60	88	(Shchelkunov *et al.*, 1995)
055R	47695	273	31.9	**31.9k protein**				(Earl *et al.*, 1986)
E8R	48516	273		VAC	4.5e-195	272/273	99	(Goebel *et al.*, 1990)
E8R		273		VAR	9.9e-192	266/273	99	(Shchelkunov *et al.*, 1993a),
MC038R		276		MCV subtype 1	8.3e-109	94/152	97	(Senkevich *et al.*, 1997)
056L	51543	1006	116.9	**DNA polymerase**				(Earl *et al.*, 1986)
E9L	48523	1006		VAC	0.0	1005/10	99	(Goebel *et al.*, 1990),
E9L		1005		VAR BSH	0.0	06	98	(Shchelkunov *et al.*, 1995)
		1008		Orf virus	0.0	598/608	51	(Mercer *et al.*, 1996)
		988		FPV	0.0	199/388	60	(Binns *et al.*, 1987)
MC039L		1004		MCV subtype 1	0.0	179/294	58	(Senkevich *et al.*, 1997)
		964		C. biennis poxvirus DNA polymerase family	2.6e-77 >6.0e-06	175/297 28/82	34	(Mustafa and Yuen, 1991)
057R	51575	95	10.9	**10.9k protein**				(Goebel *et al.*, 1990)
E10R	51862	95		VAC	1.2e-65	93/95	97	(Goebel *et al.*, 1990)
E10R		95		VAR	3.1e-64	90/95	100	(Shchelkunov *et al.*, 1993a)
MC040R		101		MCV subtype 1	5.2e-44	58/95	94	(Senkevich *et al.*, 1997)
058L	52246	129	14.9	**14.9k protein**				(Goebel *et al.*, 1990)
E11L	51857	129		VAC	3.3e-89	129/129	100	(Goebel *et al.*, 1990)
E11L		129		VAR	4.2e-87	125/129	96	(Shchelkunov *et al.*, 1995)
MC041L		132		MCV subtype 1	1.8e-30	31/96	32	(Senkevich *et al.*, 1997)
059L	52691	152	17.6	**77.6k protein (f1)**				(Goebel *et al.*, 1990)
O1L	52233	666		VAC	6.9e-101	151/152	99	(Goebel *et al.*, 1990),
Q1L		666		VAR-BSH	3.4e-92	137/152	90	(Shchelkunov *et al.*, 1995)
MC042L		783		MCV subtype 1	1.5e-22	39/105	37	(Senkevich *et al.*, 1997)
				leu zipper, bipartite nuclear targeting sequence				(Goebel *et al.*, 1990)
060L	54189	405	47.4	**77.6k protein (f2)**				(Goebel *et al.*, 1990)
O1L	52972	666		VAC	5.8e-277	399/400	99	(Goebel *et al.*, 1990)
Q1L		666		VAR-I	1.7e-269	383/400	95	(Shchelkunov *et al.*, 1995)
MC042L		783		MCV subtype 1	2.7e-51	38/104	36	(Senkevich *et al.*, 1997)

061L	54555	108	12.4	glutaredoxin 1				(Ahn and Moss, 1992a)
	54229							(Johnson *et al.*, 1991)
O2L		108		VAC	2.0e-74	108/108	100	(Goebel *et al.*, 1990)
Q2L		108		VAR	4.9e-72	104/108	96	(Shchelkunov *et al.*, 1995)
		106		human glutaredoxin	3.2e-31	49/106	46	(Fernando *et al.*, 1994)
				glutaredoxin family	>9.0e-05			
062L	55639	312	35.9	35.9k protein				(Schmitt and Stunnenberg, 1988)
I1L	54701	312		VAC	4.7e-208	310/312	99	(Goebel *et al.*, 1990)
K1L		312		VAR-BSH	4.8e-205	305/312	97	(Shchelkunov *et al.*, 1995)
MC044L		310		MCV subtype 1	3.8e-110	163/307	53	(Senkevich *et al.*, 1996)
		1451		transcription initiation protein (S. cerevisiae)	0.029	10/28	35	(Hansen *et al.*, 1996)
063L	55867	73	8.5	8.5k protein				(Schmitt and Stunnenberg, 1988)
I2L	55646	73		VAC	5.5e-50	73/73	100	(Goebel *et al.*, 1990)
K2L		73		VAR	5.5e-50	73/73	100	(Shchelkunov *et al.*, 1995)
MC045L		72		MCV subtype 1	3.5e-18	20/33	60	(Senkevich *et al.*, 1996)
		887		hypothetical yeast protein	8.1e-05	9/24	37	S48422
064L	56677	269	30.0	DNA binding phospho-protein (F4L interacting)				(Schmitt and Stunnenberg, 1988)
	55868							(Davis and Mathews, 1993)
I3L		269		VAC	2.1e-173	267/269	99	(Goebel *et al.*, 1990)
K3L		269		VAR	2.5e-172	265/269	98	(Shchelkunov *et al.*, 1995)
MC046L		288		MCV subtype 1	9.6e-66	61/149	40	(Senkevich *et al.*, 1996)
		209		FPV I3 protein	8.4e-35	23/66	34	A48563
065L	59075	771	87.8	ribonucleotide reductase (large subunit)				(Schmitt and Stunnenberg, 1988)
	56760							(Tengelsen *et al.*, 1988)
I4L		771		VAC	0.0	771/771	100	(Goebel *et al.*, 1990)
K4L		771		VAR	0.0	761/771	98	(Shchelkunov *et al.*, 1995)
				ribonucleotide red. family	>1.8e-05			
066L	59342	79	8.8	8.8k protein				(Schmitt and Stunnenberg, 1988)
I5L	59103	79		VAC	6.3e-49	79/79	100	(Goebel *et al.*, 1990)
K5L		79		VAR	1.2e-47	76/79	96	(Shchelkunov *et al.*, 1995)
MC047L		82		MCV subtype 1	2.6e-17	27/73	36	(Senkevich *et al.*, 1996)
		81		FPV 9.1k protein	1.4e-12	13/38	34	(Binns *et al.*, 1988)
		321		formate dep. nitrit reductase protein (H. influenzae)	0.00022	7/18	38	(Fleischmann *et al.*, 1995)
		496		permease (b. subtilis)	0.00031	12/43	27	gi:2415386
067L	60509	382	43.5	43.5k protein				(Schmitt and Stunnenberg, 1988)
I6L	59361	382		VAC	8.6e-268	382/382	100	(Goebel *et al.*, 1990)
K6L		382		VAR	3.1e-267	380/382	99	(Shchelkunov *et al.*, 1995)
MC048L		406		MCV subtype 1	2.1e-99	44/119	36	(Senkevich *et al.*, 1996)

ORF[a]	START STOP	AA[b]	kDa[c]	name / (putative) function / homologies[e]	BLAST[d] expect	BLAST[e] AA id	HSS[f] (%)	references
left terminal region:								
		390		FPV I6 protein mitochondrial energy transfer proteins signature	1.4e-86	50/136	36	E48563, P12925 (Goebel *et al.*, 1990)
068L	61773 60502	423	49.0	core protein, topoisomerase II				(Schmitt and Stunnenberg, 1988) (Kane and Shuman, 1993)
I7L		423		VAC	0.0	420/423	99	(Goebel *et al.*, 1990)
K7L		423		VAR	1.5e-306	419/423	99	(Shchelkunov *et al.*, 1995)
MC049L		515		MCV subtype 1	1.9e-199	126/207	60	(Senkevich *et al.*, 1996)
		421		FPV I7 protein	8.1e-180	185/340	54	F48563
		464		Amsacta moorei poxvirus	3.2e-14	14/47	29	(Hall and Moyer, 1991)
069R	61776 63809	676	77.6	NPH-II, NTPase, RNA helicase				(Shuman, 1992), (Koonin and Senkevich, 1992)
I8R		676		VAC	0.0	674/676	99	(Goebel *et al.*, 1990)
K8R		676		VAR	0.0	665/676	98	(Shchelkunov *et al.*, 1995)
MC050R		684		MCV subtype 1	7.6e-227	144/272	52	(Senkevich *et al.*, 1997)
		682		FPV virus I8FPV	4.2e-206	98/178	55	(Binns *et al.*, 1988)
				61 matches mainly to RNA helicase family	<0.38			
070L	65588	591	68.0	68k protein				(Schmitt and Stunnenberg, 1988)
G1L	63813	591		VAC	0.0	590/591	99	(Goebel *et al.*, 1990)
H1L		591		VAR-1	0.0	582/591	98	(Shchelkunov *et al.*, 1995)
MC056L		593		MCV subtype 1	1.2e-217	183/361	50	(Senkevich *et al.*, 1997)
		341		FPV	9.4e-75	45/101	44	H48563
071L	65920 65585	111	12.8	12.8k protein				(Schmitt and Stunnenberg, 1988) (Meis and Condit, 1991)
G3L		111		VAC	7.6e-74	111/111	100	(Goebel *et al.*, 1990)
H3L		111		VAR	2.4e-71	108/111	97	(Shchelkunov *et al.*, 1995)
MC057L		108		MCV subtype 1	0.00012	15/45	33	(Senkevich *et al.*, 1997)
072R	65914	220	25.8	IBT-dependent protein				(Meis and Condit, 1991)
G2R	66576	220		VAC	1.9e-155	220/220	100	(Goebel *et al.*, 1990)
H2R		220		VAR	1.1e-151	214/220	97	(Shchelkunov *et al.*, 1995)
MC058R		246		MCV subtype 1	2.7e-36	42/135	31	(Senkevich *et al.*, 1997)
073L	66920 66546	124	14.0	glutaredoxin 2 membrane protein				(Gvakharia *et al.*, 1996) (Jensen *et al.*, 1996)
H4L		124		VAR	4.0e-83	123/124	99	(Shchelkunov *et al.*, 1995)
G4L		124		VAC	7.5e-83	123/124	99	(Goebel *et al.*, 1990)
MC059L		126		MCV subtype 1	1.1e-21	21/51	41	(Senkevich *et al.*, 1997)
074R	66923	434	49.9	49.8k protein				(Goebel *et al.*, 1990)
G5R	68227	434		VAC	1.6e-305	432/434	99	(Goebel *et al.*, 1990)
H5R		434		VAR	1.9e-299	423/434	97	(Shchelkunov *et al.*, 1995)
MC60R		437		MCV subtype 1	1.0e-55	56/119	47	(Senkevich *et al.*, 1997)
		1300		HS CG1 protein	0.015	22/82	26	(Print *et al.*, 1994)

075R	68235	63	7.3	**RNA polymerase subunit rpo7**				(Amegadzie *et al.*, 1992), (Meis and Condit, 1991)
	68426							
G5.5R		63		VAC	1.1e-40	63/63	100	(Goebel *et al.*, 1990)
H5.5R		63		VAR	1.1e-39	61/63	96	(Shchelkunov *et al.*, 1995)
MC061R		63		MCV subtype 1	9.3e-27	41/63	65	(Senkevich *et al.*, 1997)
				35 matches mainly to RNA polymerases	<0.54			
076R	68428	165	19.0	**18.9k protein**				(Goebel *et al.*, 1990)
G6R	68925	165		VAC	3.8e-116	162/165	98	(Goebel *et al.*, 1990)
H6R		165		VAR	1.5e-116	164/165	99	(Shchelkunov *et al.*, 1995)
MC062R		195		MCV subtype 1	3.0e-32	27/57	47	(Senkevich *et al.*, 1997)
077L	70005	371	42.0	**42.0k protein**				(Schmitt and Stunnenberg, 1988)
G7L	68890	371		VAC	5.2e-255	370/371	99	(Goebel *et al.*, 1990)
H7L		371		VAR	7.1e-255	369/371	99	(Shchelkunov *et al.*, 1995)
MC065L		402		MCV subtype 1	2.0e-109	69/145	47	(Senkevich *et al.*, 1997)
078R	70036	260	29.9	**VLTF-1, late transcription factor**				(Keck *et al.*, 1990)
	70818							(Wright *et al.*, 1991)
G8R		260		VAC	8.6-184	259/260	99	(Goebel *et al.*, 1990)
H8R		260		VAR-I	3.1e-183	258/260	99	(Shchelkunov *et al.*, 1995)
MC067R		260		MCV subtype 1	8.5e-136	185/260	71	(Senkevich *et al.*, 1997)
		260		FPV virus FPO	3.3e-129	175/250	67	(Binns *et al.*, 1988)
079R	70838	340	38.9	**37k myristylprotein**				(Martin *et al.*, 1997)
G9R	71860	340		VAC	3.7e-237	317/319	99	(Goebel *et al.*, 1990)
H9R		340		VAR	9.1e-236	315/319	98	(Shchelkunov *et al.*, 1995)
MC068R		342		MCV subtype 1	4.8e-79	59/127	46	(Senkevich *et al.*, 1997)
		336		FPV virus FP1	3.9e-65	59/124	47	(Binns *et al.*, 1988)
080R	71861	250	27.3	**25k myristylprotein IMV virion protein**				(Franke *et al.*, 1990)
	72613							(Martin *et al.*, 1997)
L1R		250		VAC	1.8e-175	250/250	100	(Goebel *et al.*, 1990)
M1R		250		VAR	6.4e-170	249/250	99	(Shchelkunov *et al.*, 1995)
MC069R		243		MCV subtype 1	6.5e-103	145/243	59	(Senkevich *et al.*, 1997)
		243		FPV virus FP2	6.2e-95	128/243	52	(Binns *et al.*, 1988)
		212		VAC F9L	1.6e-0.7	20/58	34	(Goebel *et al.*, 1990)
		212		VAR C13L	3.1e-0.7	20/58	34	(Shchelkunov *et al.*, 1995)

GENOMIC SEQUENCE OF THE MVA STRAIN

ORF[a]	START STOP	AA[b]	kDa[c]	name / (putative) function / homologies[g]	BLAST[d] expect	BLAST[e] AA id	HSS[f] (%)	references
left terminal region:								
		213		MCV subtype 1 MC016L	1.6e-0.7	13/57	22	(Senkevich *et al.*, 1997)
		215		swinepox	3.3e-0.5	15/51	29	(Massung *et al.*, 1993)
081R	72645	87	10.3	**10.3k protein**				(Plucienniczak *et al.*, 1985)
L2R	72908	87		VAC	3.9e-57	87/87	100	(Goebel *et al.*, 1990)
M2R		87		VAR	4.0e-56	85/87	97	(Shchelkunov *et al.*, 1995)
MC070R		93		MCV subtype 1	0.064	18/80	22	(Senkevich *et al.*, 1997)
		504		Na^+ dependent phosphate transporter C. elegans	6.9e-05	10/39	25	(Wilson *et al.*, 1994)
		233		ATPase subunit T. cruzi	0.013	16/44	36	U38184
		2336		Ca^{2+} channel rat	5.2e+0.2	6/25	24	(Dubel *et al.*, 1992)
		2238		Ca^{2+} channel mouse	7.1e+0.2	6/25	24	(Coppola *et al.*, 1994)
		1559		ABC transporter yeast	0.40	12/40	30	X97560
082L	73950	350	40.6	**40.6k protein**				(Plucienniczak *et al.*, 1985)
L3L	72898	350		VAC	2.2e-251	346/350	98	(Goebel *et al.*, 1990)
M3L		349		VAR	1.5e-241	296/306	96	(Shchelkunov *et al.*, 1995)
MC072L		310		MCV subtype 1	1.5e-88	64/136	47	(Senkevich *et al.*, 1997)
		301		FPV F4 prolein	1.1e-80	58/134	43	(Binns *et al.*, 1988)
083R	73975 74730	251	28.5	**core protein VP8 DNA/RNA binding protein**				(Yang and Bauer, 1988) (Baylis and Smith, 1997)
L4R		251		VAC	5.6e-170	251/251	100	(Goebel *et al.*, 1990)
M4R		251		VAR	3.7-169	250/251	99	(Shchelkunov *et al.*, 1995)
MC073R		254		MCV subtype 1	1.7e-76	36/59	61	(Senkevich *et al.*, 1997)
		253		FPV virus FP5	6.4e-55	29/57	50	(Binns *et al.*, 1988)
084R	74740	128	15.1	**15.1k protein**				
L5R	75126	128		VAC 14.0k protein	2.9e-89	127/128	99	(Goebel *et al.*, 1990)
M5R		128		VAR	2.0-87	125/128	97	(Shchelkunov *et al.*, 1995)
-		129		FPV FP6	8.1e-16	19/45	42	(Drillien *et al.*, 1987)
MC074R		146		MCV subtype 1	0.073	10/18	55	(Senkevich *et al.*, 1997)
		152		melatonin receptor D. rerio	0.44	15/66	222	(Reppert *et al.*, 1995)
085R	75083	153	17.9	**dimeric virion protein**				(Holzer & Falkner, unpubl.)
J1R	75544	153		VAC	6.0e-103	152/153	99	(Goebel *et al.*, 1990)
L1R		159		VAR-1	1.4e-101	149/153	97	(Shchelkunov *et al.*, 1995)
		147		capripox CF7	6.5e-54	53/90	58	(Gershon and Black, 1989b)
		148		myxoma MF7	4.8e-51	54/93	58	(Jackson and Bults, 1992)
		183		MCV subtype 1	1.9e-47	47/93	50	(Senkevich *et al.*, 1997)
MC075R		148		FPV FP7	1.3e-35	37/84	44	(Drillien *et al.*, 1987)
086R	75560 76093	177	20.0	**thymidine kinase**				(Hruby and Ball, 1982) (Weir and Moss, 1983)
J2R		177		VAC	5.7e-125	175/177	98	(Goebel *et al.*, 1990)
L2R		177		VAR	2.7e-122	170/177	96	(Shchelkunov *et al.*, 1995)
				38 matches mainly to thymidine kinase family	<0.18			

087R	76159	333	38.9	**poly(A) polymerase su, 2'methyl transferase**				(Gershon *et al.*, 1991)
	77160							(Gershon and Moss, 1993)
J3R		333		VAC	8.7e-136	330/333	99	(Goebel *et al.*, 1990)
L3R		333		VAR-BSH	9.8e-233	326/333	97	(Shchelkunov *et al.*, 1995)
		338		myxoma	5.7e-288	247/333	74	(Jackson and Bults, 1990)
MC076R		343		MCV subtype 1	1.4e-135	79/144	54	(Senkevich *et al.*, 1997)
		308		FPV VP39	1.7e-96	125/267	46	(Binns *et al.*, 1988)
088R	77075	185	21.3	**RNA pol subunit rpo22**				(Broyles and Moss, 1986)
J4R	77632	185		VAC	1.2e-125	185/185	100	(Goebel *et al.*, 1990)
L4R		185		VAR-BSH	7.9e-125	182/185	98	(Shchelkunov *et al.*, 1995)
		185		myxoma	1.5e-86	124/185	67	(Jackson and Bults, 1990)
MC077R		187		MCV subtype 1	1.9e-76	73/132	55	(Senkevich *et al.*, 1997)
		186		FPV	2.1e-73	72/135	53	(Binns *et al.*, 1988)
089L	78101	133	15.2	**15.2k protein**				(Plucienniczak *et al.*, 1985)
J5L	77700	133		VAC	2.4e-95	133/133	100	(Goebel *et al.*, 1990)
L5L		133		VAR-I	2.4e-94	131/133	98	(Shchelkunov *et al.*, 1995)
MC078L		134		MCV subtype 1	5.7e-45	60/127	47	(Senkevich *et al.*, 1997)
		137		FPV	1.4e-43	60/130	46	(Drillien *et al.*, 1987)
		377		VAR-I A16L (BSH:A17L)	0.049	7/28	25	(Shchelkunov *et al.*, 1995)
		378		VAC A16L	0.049	7/28	25	(Goebel *et al.*, 1990)
090R	78207	1286	146.9	**RNA pol subunit rpo147**				(Broyles and Moss, 1986)
J6R	82067	1286		VAC	0.0	1283/1286	99	(Goebel *et al.*, 1990)
L6R		1286		VAR	0.0	1275/1286	99	(Shchelkunov *et al.*, 1995)
MC079R		1289		MCV subtype 1	0.0	556/760	73	(Senkevich *et al.*, 1997)
				100 matches to RNA pol (large subunit) family	<3.7e-07			
091L	82579	171	19.7	**protein tyrosine/serine phosphatase**				(Rosel *et al.*, 1986)
	82064							(Guan *et al.*, 1991)
H1L		171		VAC	2.0e-117	170/171	99	(Goebel *et al.*, 1990)
I1l		171		VAR	1.1e-114	166/171	97	(Shchelkunov *et al.*, 1995)
		171		racoonpox	6.0e-111	157/171	91	B47452
		172		myxoma virus	1.5e-77	83/138	60	(Mossman *et al.*, 1995a)
		173		rabbit fibroma virus	1.8e-77	46/80	57	(Mossman *et al.*, 1995a)
MC082L		169		MCV subtype 1	1.4e-65	60/114	52	(Senkevich *et al.*, 1997)
				protein phosphatase family	>2.8e-05			

ORF[a]	START STOP	AA[b]	kDa[c]	name / (putative) function / homologies[g]	BLAST[d] expect	BLAST[e] AA id	HSS[f] (%)	references
left terminal region:								
092R	82593	189	21.5	**21.5k protein**				(Rosel *et al.*, 1986)
H2R	83162	189		VAC	5.2e-134	188/189	99	(Goebel *et al.*, 1990)
I2R		189		VAR	1.4e-133	188/189	99	(Shchelkunov *et al.*, 1995)
MC083R		191		MCV subtype 1	1.4e-71	95/181	52	(Senkevich *et al.*, 1997)
		142		myxoma	1.3e-65	93/142	65	(Jackson and Bults, 1990)
093L	84139 83165	324	37.5	**immunodominant env protein p35; IMV membrane-associated**				(Rosel *et al.*, 1986) (Chertov *et al.*, 1991) (Takahashi *et al.*, 1994)
H3L		324		VAC	3.3e-231	322/324	99	(Goebel *et al.*, 1990)
I3L		325		VAR-BSH	1.7e-225	311/320	97	(Shchelkunov *et al.*, 1995)
MC084L		298		MCV subtype 1	1.1e-36	38/117	32	(Senkevich *et al.*, 1996)
094L	86527 84140	795	93.6	**RAP 94 (RNA-pol assoc. transcr. spec. factor)**				(Ahn and Moss, 1992b) (Kane and Shuman, 1992)
H4L		795		VAC	0.0	791/795	99	(Goebel *et al.*, 1990)
I4L		795		VAR	0.0	780/795	98	(Shchelkunov *et al.*, 1995)
MC085L		791		MCV subtype 1	0.0	327/546	59	(Senkevich *et al.*, 1996)
		804		Orf virus	0.0	96/131	73	(Fleming *et al.*, 1993)
		484		FPV L1L protein	2.4e-181	91/176	51	2209386A
095R	86713 87324	203	22.3	**late transcription factor VLTF-4**				(Kovacs and Moss, 1996) (Rosel *et al.*, 1986)
H5R		203		VAC	1.8e-128	202/203	99	(Goebel *et al.*, 1990)
I5R		221		VAR	5.1e-102	91/97	93	(Shchelkunov *et al.*, 1995)
		227		orf virus F3R	3.1e-14	29/69	42	(Fleming *et al.*, 1993)
		220		MCV subtype 1	3.1e-09	28/64	43	(Senkevich *et al.*, 1997)
		705		nucleolin Xenopus	0.00041	18/57	31	(Messmer and Dreyer, 1993)
				31 matches to glu/asp rich proteins	E<0.52			
096R	87325 88269	314	36.7	**DNA topoisomerase I**				(Shuman and Moss, 1987) (Rosel *et al.*, 1986)
H6R		314		VAC	0.0	314/314	100	(Goebel *et al.*, 1990)
I6R		314		VAR-BSH	9.5e-220	312/314	99	(Shchelkunov *et al.*, 1995)
		314		shope fibroma virus	8.5e-141	119/170	70	(Upton *et al.*, 1990b)
		318		orf virus	5.2e-128	82/138	59	(Fleming *et al.*, 1993)
MC087R		323		MCV subtype 1	1.6e-121	111/202	54	(Senkevich *et al.*, 1997)
		316		FPV L3R	2.9e-113	159/303	52	(Zantinge *et al.*, 1996)
				21 matches to topoisomerase family				
097R	88306	146	17.0	**17.0k protein**				(Rosel *et al.*, 1986)
H7R	88746	146		VAC	2.1e-98	144/146	98	(Goebel *et al.*, 1990)
I7R		146		VAR	6.7e-96	141/146	96	(Shchelkunov *et al.*, 1995)
MC088R		143		MCV subtype 1	4.3e-30	45/115	39	(Senkevich *et al.*, 1997)

098R	88790	844	96.8	**mRNA capping enzyme,**				(Morgan *et al.*, 1984)
	91324			**large subunit**				(Niles *et al.*, 1986)
D1R		844		VAC	0.0	842/844	99	(Goebel *et al.*, 1990)
F1R		844		VAR-BSH	0.0	830/844	98	(Shchelkunov *et al.*, 1995)
MC090R		950		MCV subtype 1	0.0	322/64	64	(Senkevich *et al.*, 1997)
		836		shope fibroma virus	0.0	243/305	79	(Upton *et al.*, 1991b)
		868		ASV NP868R	0.0033	17/55	30	(Pena *et al.*, 1993)
099L	91723	146	16.9	**structural protein**				(Niles *et al.*, 1986)
	91283							(Dyster and Niles, 1991)
D2L		146		VAC	5.9e-98	146/146	100	(Goebel *et al.*, 1990)
F2L		146		VAR (BSH: F3L)	1.5e-97	145/146	99	(Shchelkunov *et al.*, 1995)
		143		Rabbit fibroma virus	2.0e-27	13/33	39	(Upton *et al.*, 1991b)
MC091L		170		MCV subtype 1	1.1e-20	19/41	46	(Senkevich *et al.*, 1996)
100R	91716	233	27.6	**27k structural protein**				(Dyster and Niles, 1991)
D3R	92417	237		VAC	3.8-167	136/142	95	(Goebel *et al.*, 1990)
F2R		237		VAR I:F3R	1.5e-162	131/142	92	(Shchelkunov *et al.*, 1995)
		241		shope fibroma virus	9.3e-20	27/100	27	(Upton *et al.*, 1991b)
MC092R		268		MCV subtype 1	3.5e-18	16/39	41	(Senkevich *et al.*, 1997)
		206		rabbit fibroma virus C3	1.6e-09	26/96	27	(Strayer *et al.*, 1991)
101R	92417	218	25.1	**uracil DNA glycosylase**				(Upton *et al.*, 1993)
D4R	93073	218		VAC	1.4e-157	217/218	99	(Goebel *et al.*, 1990)
F4R		218		VAR-BSH	5.1e-157	216/218	99	(Shchelkunov *et al.*, 1995)
		218		shope fibroma virus	1.5e-117	151/218	69	(Upton *et al.*, 1993)
MC093R		226		MCV subtype 1	8.4e-91	65/113	57	(Senkevich *et al.*, 1997)
		218		FPV FPD4	3.1e-88	116/216	53	(Tartaglia *et al.*, 1990)
		297		uracil DNA glycosylase UL2 gallid herpesvirus 1	0.019	8/14	57	L34064
102R	93105	785	90.4	**90.4k ATP/GTP binding**				(Niles *et al.*, 1986)
	95462			**protein**				(Shchelkunov *et al.*, 1993c)
D5R		785		VAC	0.0	780/785	99	(Goebel *et al.*, 1990)
F5R		785		VAR	0.0	774/785	98	(Shchelkunov *et al.*, 1995)
		786		shope fibroma C5	0.0	283/450	62	(Strayer *et al.*, 1991)
		791		MCV subtype 1	0.0	184/334	55	(Senkevich *et al.*, 1997)
		791		FPV virus FPD5	0.0	170/345	49	(Tartaglia *et al.*, 1990)
MC094R		942		C29E6.4 C. elegans	0.72	16/56	28	(Wilson *et al.*, 1994)
103R	95503	637	73.9	**early transcription factor**				(Broyles and Fesler, 1990)
	97416			**VETF-1**				(Gershon and Moss, 1990)

GENOMIC SEQUENCE OF THE MVA STRAIN

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left terminal region:								
D6R		637		VAC	0.0	635/637	99	(Goebel *et al.*, 1990)
F6R		637		VAR-I	0.0	633/637	99	(Shchelkunov *et al.*, 1995)
		635		shope fibroma virus	0.0	212/262	80	(Strayer *et al.*, 1991)
MC095R		635		MCV subtype I	0.0	199/263	75	(Senkevich *et al.*, 1997)
		605		FPV	0.0	188/263	71	(Binns *et al.*, 1990)
								(Tartaglia *et al.*, 1990)
		648		Choristoneura biennis EPV	2.7e-08	24/72	33	(Yuen *et al.*, 1991)
		648		Amsacta moorei EPV	4.2e-06	24/77	31	(Hall and Moyer, 1991)
		706		African swine fever virus	1.5e-05	13/38	34	(Yanez *et al.*, 1993)
104R	97443 97928	161	17.9	**RNA polymerase subunit rpo18**				(Ahn *et al.*, 1990b) (Quick and Broyles, 1990)
D7R		161		VAC	1.4e-108	160/161	99	(Goebel *et al.*, 1990)
F7R		161		VAR	2.2e-106	156/161	96	(Shchelkunov *et al.*, 1995)
		163		rabbit fibroma C8	3.4e-76	108/161	67	(Strayer *et al.*, 1991)
MC097R		161		MCV subtype I	4.0e-70	99/158	62	(Senkevich *et al.*, 1997)
		161		FPV D7	5.4e-66	95/160	59	(Binns *et al.*, 1990)
105L	98805 97891	304	35.4	**virion transmembrane protein, carbonic anhydrase-like**				(Niles and Seto, 1988) (Niles *et al.*, 1986) (Maa *et al.*, 1990)
D8L		304		VAC	2.3e-212	297/304	97	(Goebel *et al.*, 1990)
F8L		304		VAR	2.5e-209	291/304	95	(Shchelkunov *et al.*, 1995)
		304		Camelpox virus	1.1e-207	290/304	95	X97857
		303		Ectromelia virus	2.2e-207	195/207	94	X97856
		304		Monkeypox virus	3.0e-207	287/304	94	X97855
		304		Cowpox virus	9.8e-206	285/304	93	X97858
				Carbonic anhydrase family	>4.9e-13			
106R	98847 99488	213	25.0	**25k mutT-like protein**				(Koonin, 1993) (Niles *et al.*, 1986)
D9R		213		VAC	1.6e-146	212/213	99	(Goebel *et al.*, 1990)
F9R		213		VAR	5.3e-145	209/213	98	(Shchelkunov *et al.*, 1995)
		218		rabbit fibroma	1.7e-75	105/203	51	(Strayer *et al.*, 1991)
MC098R		212		MCV subtype I	5.3e-67	54/111	48	(Senkevich *et al.*, 1997)
		78		FPV D9	2.0e-13	25/51	49	(Tartaglia *et al.*, 1990)
MC099R		229		MCV subtype I	0.0041	13/31	41	(Senkevich *et al.*, 1997)
		248		VAR-I F10R	0.018	14/32	43	(Shchelkunov *et al.*, 1995)
		225		FPV D10	0.14	15/34	44	(Tartaglia *et al.*, 1990)
		248		VAC D10R	0.23	11/26	42	(Goebel *et al.*, 1990)

107R	99485 100231	248	28.9	**29k mutT-like protein**				(Koonin, 1993) (Niles *et al.*, 1986)
D10R		248		VAC	7.4e-173	245/248	98	(Goebel *et al.*, 1990)
F10R		248		VAR-1	5.4e-173	245/248	98	(Shchelkunov *et al.*, 1995)
		260		shope fibroma D10	3.8e-72	96/202	47	(Strayer *et al.*, 1991)
MC099R		229		MCV subtype 1	1.4e-54	44/100	44	(Senkevich *et al.*, 1997)
		225		FPV D10	1.1e-45	45/102	44	(Binns *et al.*, 1990)
		218		shope fibroma D9	1.9e-06	19/54	35	(Strayer *et al.*, 1991)
		212		MCV subtype 1 MC098R	0.13	12/21	57	(Senkevich *et al.*, 1997)
		136		mutator Synechocystis	0.23	12/27	44	D90899
		213		VAC D9R	0.24	11/26	42	(Goebel *et al.*, 1990)
		213		VAR F9R	0.24	11/26	42	(Shchelkunov *et al.*, 1995)
		169		mutator M. jannaschii	0.39	13/25	52	(Bult *et al.*, 1996)
108L	102127 100232	631	72.4	**nucleoside triphosphate phosphohydrolase I, DNA helicase**				(Broyles and Moss, 1987) (Rodriguez *et al.*, 1986) (Koonin and Senkevich, 1992)
D11L		631		VAC	0.0	629/631	99	(Goebel *et al.*, 1990)
N1L		631		VAR	0.0	626/631	99	(Shchelkunov *et al.*, 1995)
MC100R		634		MCV subtype 1	7.3e-286	392/627	62	(Senkevich *et al.*, 1996)
		637		FPV protein 5	2.8e-275	214/357	59	S42251
		370		Rabbit fibroma C14 protein	1.8e-176	244/368	66	F36819
		648		AmEPV	6.0e-142	81/159	50	(Hall and Moyer, 1991)
		648		Choristoneura biennis EPV	1.1e-136	81/158	51	(Yuen *et al.*, 1991)
		89		Swinepox virus	1.2e-34	60/89	67	(Massung *et al.*, 1993)
		1098		ASF	1.6e-13	26/89	29	(Baylis *et al.*, 1993)
		1085		RAD26 (yeast)	5.1e-05	16/45	35	(Huang *et al.*, 1994)
		769		HS transcription activator NTPase family	0.00093 >5.1e-5	10/22	45	(Okabe *et al.*, 1992)
109L	103025 102162	287	33.3	**mRNA capping enzyme, transcription initiation factor VITF**				(Niles *et al.*, 1989) (Weinrich and Hruby, 1986) (Vos *et al.*, 1991)
D12L		287		VAC	2.0e-198	285/287	99	(Goebel *et al.*, 1990)
N2L		287		VAR	9.8e-198	284/287	99	(Shchelkunov *et al.*, 1995)
-		287		Swinepox virus	4.1e-160	220/287	76	(Massung *et al.*, 1993)
MC101L		295		MCV subtype 1	5.8e-126	171/279	61	(Senkevich *et al.*, 1996)
		289		FPV protein 6	3.4e-113	114/215	53	S42252
110L	104711 103056	551	61.9	**rifampicin resistance gene, IMV protein**				(Tartaglia and Paoletti, 1985) (Weinrich and Hruby, 1986)
D13L		551		VAC	0.0	551/551	100	(Goebel *et al.*, 1990)
N3L		551		VAR	0.0	547/551	99	(Shchelkunov *et al.*, 1995)
		551		Swinepox virus	4.5e-286	357/506	70	(Massung *et al.*, 1993)
MC102L		547		MCV subtype 1	5.4e-248	298/494	60	(Senkevich *et al.*, 1996)
		552		FPV protein 7	6.6e-223	182/305	59	S42253
		584		Heliothis armigera EPV	9.5e-51	54/107	50	(Osborne *et al.*, 1996)

ORF[a]	START STOP	AA[b]	kDa[c]	name / (putative) function / homologies[g]	BLAST[d] expect	BLAST[e] AA id	HSS[f] (%)	references
left terminal region:								
111L	105187	150	16.9	late gene trans-activator,				(Weinrich and Hruby, 1986)
	104735			VLTF-2				(Keck *et al.*, 1993)
A1L		150		VAC	6.8e-103	149/150	99	(Goebel *et al.*, 1990)
A1L		150		VAR	6.8e-103	149/150	99	(Shchelkunov *et al.*, 1995)
MC103L		169		MCV subtype 1	6.3e-54	74/147	50	(Senkevich *et al.*, 1996)
		154		FPV protein 8	2.8e-50	50/87	57	S42254
112L	105882	224	26.3	late gene trans-activator				(Weinrich and Hruby, 1986)
A2L	105208			VAC				(Passarelli *et al.*, 1996)
A2L		224		VAR	1.3e-158	224/224	100	(Goebel *et al.*, 1990)
MC104L		224		MCV subtype 1	1.3e-158	224/224	100	(Shchelkunov *et al.*, 1995)
		228		orf virus	6.4e-127	172/222	77	(Senkevich *et al.*, 1996)
		606			6.8e-30	43/66	65	(Mercer *et al.*, 1995)
113L	106109	76	8.9	8.9k protein				
	105879	76		VAC-WR	1.6e-47	73/76	96	(Weinrich and Hruby, 1986)
A3L		76		VAR-BSH (I:A2.5L)	2.1e-47	71/76	93	(Shchelkunov *et al.*, 1995)
MC105L		70		MCV subtype 1	9.8e-12	26/63	41	(Senkevich *et al.*, 1996)
114L	108058	644	72.6	major core protein P4b				(Rosel and Moss, 1985)
A3L	106124	644		VAC	0.0	643/644	99	(Goebel *et al.*, 1990)
A4L		644		VAR-BSH (I:A3L)	0.0	636/644	98	(Shchelkunov *et al.*, 1995)
MC106L		675		MCV subtype 1	8.9e-272	227/357	63	(Senkevich *et al.*, 1996)
		657		FPV Major core protein P4b	9.1e-220	169/299	56	(Binns *et al.*, 1989)
115L	108929	272	29.9	membrane associated core				(Demkowicz *et al.*, 1992)
	108111			protein				(Cudmore *et al.*, 1996)
A4L		281		VAC	1.1e-145	180/187	96	(Goebel *et al.*, 1990)
A5L		271		VAR-BSH (I: A4L)	1.1e-112	165/178	92	(Shchelkunov *et al.*, 1995)
		268		Thermoproteus phage 1	1.9e-09	38/127	29	(Neumann and Zillig, 1990)
		5179		human mucin	4.5e-07	34/139	24	(Gum *et al.*, 1994)
				many matches to Pro-rich proteins				
116R	108967	164	19.0	RNA pol subunit rpo19				(Ahn *et al.*, 1992)
A5R	109461	164		VAC	5.8e-110	164/164	100	(Goebel *et al.*, 1990)
A5R		164		VAR-I (BSH:A6R)	7.0e-109	162/164	98	(Shchelkunov *et al.*, 1995)
MC108R		165		MCV subtype 1	3.3e-51	82/151	53	(Senkevich *et al.*, 1997)
		167		FPV	3.3e-51	72/161	44	(Kumar and Boyle, 1990)
				54 matches/glu-rich proteins	<0.51			
117L	110576	372	43.1	43.1k protein				
A6L	109458	372		VAC	1.2e-248	371/372	99	(Goebel *et al.*, 1990)
A7L		372		VAR-BSH (I: A6L)	1.1e-244	364/372	97	(Shchelkunov *et al.*, 1995)
MC109L		461		MCV subtype 1	4.0e-99	132/367	35	(Senkevich *et al.*, 1996)
		339		FPV ORF 2 protein	1.9e-95	111/279	39	B60013

118L	112732	710	82.3	**VETF 82k subunit**				(Gershon and Moss, 1990)
A7L	110600	710		VAC	0.0	708/710	99	(Goebel *et al.*, 1990)
A8L		710		VAR-BSH (I: A7L)	0.0	700/710	98	(Shchelkunov *et al.*, 1995)
MC110L		707		MCV subtype 1	0.0	240/374	64	(Senkevich *et al.*, 1996)
119R	112786	288	33.6	**33.6k protein**				(Van Meir and Wittek, 1988)
A8R	113652	288		VAC	5.3e-198	287/288	99	(Goebel *et al.*, 1990)
A8R		288		VAR-I (BSH:A9R)	3.1e-195	284/288	98	(Shchelkunov *et al.*, 1995)
MC111R		435		MCV subtype 1	4.4e-94	100/169	59	(Senkevich *et al.*, 1997)
120L	113929	94	10.5	**10.5k protein**				(Van Meir and Wittek, 1988)
A10L	113645	95		VAR-BSH (I: A9L)	9.0e-59	78/79	98	(Shchelkunov *et al.*, 1995)
A9L		99		VAC	9.4e-55	82/91	90	(Goebel *et al.*, 1990)
MC112L		128		MCV subtype 1	1.0e-29	47/71	66	(Senkevich *et al.*, 1996)
		69		orf virus	3.0e-16	27/45	60	(Mercer *et al.*, 1995)
121L	116605 113930	891	102.2	**major core protein P4a**				(Van Meir and Wittek, 1988) (Vanslyke *et al.*, 1991)
A10L		891		VAC	0.0	883/891	99	(Goebel *et al.*, 1990)
A11L		892		VAR-BSH (I: A10L)	0.0	442/463	95	(Shchelkunov *et al.*, 1995)
MC113L		889		MCV subtype 1	5.8e-289	99/177	55	(Senkevich *et al.*, 1996)
122R	116620	318	36.1	**36.1k protein**				(Goebel *et al.*, 1990)
A11R	117576	318		VAC	3.5e-212	318/318	100	(Goebel *et al.*, 1990)
A11R		319		VAR-I (BSH: A12R)	2.7e-154	242/277	87	(Shchelkunov *et al.*, 1995)
MC114R		304		MCV subtype 1	2.9e-98	92/154	59	(Senkevich *et al.*, 1997)
		148		FPV 4a gene	1.9e-13	18/32	56	A20158
123L	118141	187	20.0	**virion protein**				(Takahashi *et al.*, 1994)
A12L	117578	192		VAC	4.8e-127	127/128	99	(Goebel *et al.*, 1990)
A13L		189		VAR-BSH (I: A12L)	5.9e-64	101/144	70	(Shchelkunov *et al.*, 1995)
MC115L		178		MCV subtype 1	5.9e-37	39/83	46	(Senkevich *et al.*, 1996)
124L	118377 118165	70	7.6	**structural protein** **IMV membrane protein**				(Takahashi *et al.*, 1994) (Jensen *et al.*, 1996)
		70		**p8**	2.4e-42	66/69	95	(Goebel *et al.*, 1990)
A13L		68		VAC	4.1e-20	37/64	57	(Shchelkunov *et al.*, 1995)
A14L				VAR-BSH (I: A13L)				
125L	118757 118485	90	10.0	**structural protein** **IMV membrane protein p16**				(Takahashi *et al.*, 1994) (Jensen *et al.*, 1996)

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ORF[a]	START STOP	AA[b]	kDa[c]	name / (putative) function / homologies[g]	BLAST[d] expect	BLAST[e] AA id	HSS[f] (%)	references
left terminal region:								
A14L		90		VAC	5.3e-62	90/90	100	(Goebel *et al.*, 1990)
A15L		90		VAR-BSH (I: A14L)	5.3e-61	88/90	97	(Shchelkunov *et al.*, 1995)
MC118L		94		MCV subtype 1	7.3e-22	31/72	43	(Senkevich *et al.*, 1996)
		125		human interferon inducible protein	0.23	15/49	30	(Deblandre *et al.*, 1995)
126L	119209	94	11.0	**11k protein**				
A15L	118925	94		VAC	4.1e-63	94/94	100	(Goebel *et al.*, 1990)
A16L		94		VAR-BSH (I:A15L)	1.0e-61	92/94	97	(Shchelkunov *et al.*, 1995)
MC120L		96		MCV subtype 1	6.7e-08	17/51	33	(Senkevich *et al.*, 1996)
127L	120326	377	43.4	**35k myristylprotein**				(Martin *et al.*, 1997)
A16L	119193	378		VAC	6.3e-288	327/327	100	(Goebel *et al.*, 1990)
A17L		377		VAR-BSH (I:A16L)	1.5e-283	368/377	97	(Shchelkunov *et al.*, 1995)
MC121L		364		MCV subtype 1	6.5e-110	45/115	39	(Senkevich *et al.*, 1996)
128L	120940 120329	203	23.0	**IMV membrane protein morphogenesis factor**				(Krijnse-Locker *et al.*, 1996) (Rodriguez *et al.*, 1995) (Wolffe *et al.*, 1996)
A17L		203		VAC	1.0e-141	201/203	99	(Goebel *et al.*, 1990)
A18L		203		VAR-BSH (I:A17L)	1.0e-141	201/203	99	(Shchelkunov *et al.*, 1995)
MC122L		179		MCV subtype 1	1.4e-47	36/81	44	(Senkevich *et al.*, 1996)
129R	120955 122436	493	56.8	**DNA helicase DNA dependent ATPase**				(Koonin and Senkevich, 1992) (Bayliss and Condit, 1995)
A18R		493		VAC	0.0	488/493	98	(Goebel *et al.*, 1990)
A18R		493		VAR-I (BSH:A19R)	0.0	478/493	96	(Shchelkunov *et al.*, 1995)
MC123R		694		MCV subtype 1	5.3e-167	203/403	50	(Senkevich *et al.*, 1997)
		450		Bacteriophage T5 D10 helicase-like protein	0.0066	13/36	36	P11107
130L	122650	77	8.3	**8.3kb protein**				(Goebel *et al.*, 1990)
A19L	122417	77		VAC	2.9e-50	77/77	100	(Goebel *et al.*, 1990)
A19L		76		VAR-I (BSH: A20L)	1.2e-34	54/64	84	(Shchelkunov *et al.*, 1995)
MC124L		78		MCV subtype 1	1.5e-13	14/37	37	(Senkevich *et al.*, 1996)
		1721		HS RIZ, zink finger protein	0.0060	7/16	43	(Buyse *et al.*, 1995)
131L	123004	117	13.6	**13.6k protein**				(Goebel *et al.*, 1990)
A21L	122651	117		VAC	5.3e-83	117/117	100	(Goebel *et al.*, 1990)
A22L		117		VAR-BSH (I: A20L)	7.2e-82	115/117	98	(Shchelkunov *et al.*, 1995)
MC125L		114		MCV subtype 1	2.8e-28	23/41	56	(Senkevich *et al.*, 1996)

132R	123003	426	49.1	**49.1k protein**				(Goebel *et al.*, 1990)
A20R	124283	426		VAC	7.6e-298	423/426	99	(Goebel *et al.*, 1990)
A21R		426		VAR	1.6e-294	418/426	98	(Shchelkunov *et al.*, 1995)
MC126R		476		MCV subtype 1	3.2e-95	34/131	25	(Senkevich *et al.*, 1997)
		1118		Pichia klyveri DNA pol	0.069	12/54	22	Y11606
133R	124213	187	21.9	**21.9k protein**				(Goebel *et al.*, 1990)
A22R	124776	187		VAR-1 (BSH:A23R)	1.1e-126	182/187	97	(Shchelkunov *et al.*, 1995)
A22R		176		VAC	1.2e-122	174/176	98	(Goebel *et al.*, 1990)
MC127R		282		MCV subtype 1	5.8e-43	35/85	41	(Senkevich *et al.*, 1997)
134R	124796	382	44.6	**44.6k protein**				(Goebel *et al.*, 1990)
A23R	125944	382		VAC	4.2e-269	382/382	100	(Goebel *et al.*, 1990)
A23R		382		VARI (BSH:A24R)	1.7e-265	377/382	98	(Shchelkunov *et al.*, 1995)
MC128R		383		MCV subtype 1	3.5e-136	83/143	58	(Senkevich *et al.*, 1997)
135R	125966	1155	132.4	**RNA pol subunit rpo132**				(Hooda-Dhingra *et al.*, 1990)
	129436							(Amegadzie *et al.*, 1991b)
A24R		1164		VAC	0.0	794/796	99	(Goebel *et al.*, 1990)
		1164		CPX rpo132	0.0	794/795	99	(Patel and Pickup, 1989)
A25R		1164		VAR-BSH (I:A24R)	0.0	789/795	99	(Shchelkunov *et al.*, 1995)
MC129R		1165		MCV subtype 1	0.0	441/565	78	(Senkevich *et al.*, 1997)
		1162		orf virus	0.0	166/258	64	U33419
				101 matches to RNA pol beta subunit family	<0.036			
right terminal region:								
136L	129638	65	7.5	**150k CPX-ATI (f)**				(Funahashi *et al.*, 1988)
A25L	129441	65		VAC	1.3e-41	64/65	98	(Goebel *et al.*, 1990)
		1284		Cowpox (CPX-ATI)	3.2e-15	28/30	93	(Funahashi *et al.*, 1988)
137L	130916	230	27.1	**27.1k protein (f)**				(Amegadzie *et al.*, 1991a)
A30L	130224	498		VAR-BSH (I: A29L)	3.1e-158	216/227	95	(Shchelkunov *et al.*, 1995)
A26L		322		VAC (ATI flanking protein)	5.6e-142	195/197	98	(Goebel *et al.*, 1990)
MC131L		513		MCV subtype 1	2.1e-12	19/59	32	(Senkevich *et al.*, 1996)
MC133L		546		MCV subtype 1	4.2e-11	12/40	30	(Senkevich *et al.*, 1996)
MC130L		451		MCV subtype 1	2.3e-10	14/40	35	(Senkevich *et al.*, 1996)
		702		VAR-I A28L (BSH:A29L)	0.0021	12/37	32	(Shchelkunov *et al.*, 1995)
		726		Camelpox	0.051	11/37	29	(Meyer and Rziha, 1993)
138L	131298	110	12.5	**14k membrane protein**				(Rodriguez and Esteban, 1987)
	130966			**EEV protein**				(Rodriguez and Smith, 1990)
				fusion protein				(Gong *et al.*, 1990)
A27L		110		VAC	3.3e-70	108/110	98	(Goebel *et al.*, 1990)
A31L		110		VAR-BSH (I: /A30L)	1.1e-69	107/110	97	(Shchelkunov *et al.*, 1995)
		117		Camelpox virus	1.5e-69	106/110	96	(Meyer *et al.*, 1994)
		110		Cowpox virus	1.6e-69	107/110	97	(Meyer *et al.*, 1994)

ORF[a]	START STOP	AA[b]	kDa[c]	name / (putative) function / homologies[g]	BLAST[d] expect	BLAST[e] AA id	HSS[f] (%)	references
left terminal region:								
		110		Ectromelia virus	6.7e-68	105/110	95	(Meyer *et al.*, 1994)
		110		Monkeypox virus	8.3e-67	103/110	93	(Meyer *et al.*, 1994)
		89		Orf virus	4.8e-15	22/57	38	(Naase *et al.*, 1991)
		188		Myxoma virus	2.5e-12	18/33	54	(Jackson *et al.*, 1996)
MC133L		546		MCV subtype 1	1.5e-11	26/58	44	(Senkevich *et al.*, 1996)
		148		Capripox virus HM2 protein	2.6e-10	21/42	50	(Gershon *et al.*, 1989)
MC131L		513		MCV subtype 1	1.5e-05	18/58	31	(Senkevich *et al.*, 1996)
139L	131739	146	16.3	**16.3k protein**				(Amegadzie *et al.*, 1991a)
A28L	131299	146		VAC	1.7e-103	146/146	100	(Goebel *et al.*, 1990)
A31.5L		146		VAR-BSH (I: A31L)	2.9e-100	141/146	96	(Shchelkunov *et al.*, 1995)
		140		Myxoma virus	1.3e-55	30/52	57	(Jackson *et al.*, 1996)
		140		Capripox virus HM3 protein	3.3e-55	30/49	61	(Gershon *et al.*, 1989)
MC134L		141		MCV subtype 1	1.0e-53	31/52	59	(Senkevich *et al.*, 1996)
		143		Amsacta moorei poxvirus	2.0e-14	16/36	44	(Hall and Moyer, 1991)
140L	132657	305	35.4	**RNA pol subunit rpo35**				(Amegadzie *et al.*, 1991a)
A29L	131740	305		VAC	3.6e-215	304/305	99	(Goebel *et al.*, 1990)
A32L		305		VAR-BSH	7.5e-211	297/305	97	(Shchelkunov *et al.*, 1995)
MC135L		303		MCV subtype 1	7.0e-98	51/103	49	(Senkevich *et al.*, 1996)
		126		Capripox virus	2.2e-54	46/61	75	(Gershon *et al.*, 1989)
141L	132853	77	8.7	**8.7k protein**				(Amegadzie *et al.*, 1991a)
A30L	132620	77		VAC	5.5e-48	77/77	100	(Goebel *et al.*, 1990)
A33L		77		VAR	5.5e-48	77/77	100	(Shchelkunov *et al.*, 1995)
MC136L		67		MCV subtype 1	9.2e-16	18/40	45	(Senkevich *et al.*, 1996)
142R	133013	125	14.4	**14.4k protein**				(Smith *et al.*, 1991)
A31R	133390	124		VAC	2.0e-84	118/124	95	(Goebel *et al.*, 1990)
A34R		140		VAR	1.6e-79	111/114	97	(Shchelkunov *et al.*, 1995)
MC138R		117		MCV subtype 1	6.2e-24	39/98	39	(Senkevich *et al.*, 1997)
143L	134169 133360	269	30.8	**30.8k protein ATP/GTP binding motif A**				(Smith *et al.*, 1991) (Koonin *et al.*, 1993)
A32L		300		VAC	6.4e-190	268/269	99	(Goebel *et al.*, 1990)
A35L		270		VAR	1.6e-186	263/269	97	(Shchelkunov *et al.*, 1995)
MC140L		249		MCV subtype 1	7.6e-95	58/94	61	(Senkevich *et al.*, 1996)
144R	134287	185	20.6	**EEV glycoprotein**				(Roper *et al.*, 1996)
A33R	134844	185		VAC	2.1e-124	182/185	98	(Goebel *et al.*, 1990)
A36R		184		VAR	1.8e-121	103/112	91	(Shchelkunov *et al.*, 1995)
		185		Ectromelia	2.8e-113	165/185	89	(Roper *et al.*, 1996)
145R	134868 135374	168	19.6	**EEV glycoprotein virulence factor actin microvilli inducer**				(Duncan and Smith, 1992a) (McIntosh and Smith, 1996) (Wolffe *et al.*, 1997)
A34R		168		VAC	1.2e-117	165/168	98	(Goebel *et al.*, 1990)
A37R		168		VAR-I	1.7e-117	164/168	97	(Shchelkunov *et al.*, 1995)
		167		FPV ORFs BamHI 2,8,11 hepatic lectins homologs	<0.056	16/66	24	(Tomley *et al.*, 1988)
		199		HS early T-cell activation antigen CD69	0.0038	12/38	31	(Hamann *et al.*, 1993)
MC143R		159		MCV subtype 1 17 matches to lectins	0.080	12/48	25	(Senkevich *et al.*, 1997)

146R	135418	176	20.0	**20.0k protein**				(Smith *et al.*, 1991)
A35R	135948	176		VAC	1.4e-126	176/176	100	(Goebel *et al.*, 1990)
A38R		60		VAR-I	2.9e-37	57/60	95	(Shchelkunov *et al.*, 1995)
MC145R		233		MCV subtype 1	1.2e-07	18/55	32	(Senkevich *et al.*, 1997)
147R	136015	208	23.8k	**EEV membrane protein virulence factor**				(Parkinson and Smith, 1994)
	136641							(Smith *et al.*, 1991)
A36R		221		VAC	2.8e-143	140/141	99	(Goebel *et al.*, 1990)
A39R		216		VAR	2.1e-89	138/177	77	(Shchelkunov *et al.*, 1995)
				19 matches to asn/ser-rich proteins	<0.41			
148R	136705	263	29.8	**29.8k protein**				
A37R	137496	263		VAC	6.8e-183	261/262	99	(Goebel *et al.*, 1990)
A40R		68		VAR	4.9e-37	61/67	91	(Shchelkunov *et al.*, 1995)
149L	138589	277	31.5	**31.5k protein**				(Amegadzie *et al.*, 1991a)
A38L	137756	277		VAC	9.3e-198	274/277	98	(Goebel *et al.*, 1990)
A41L		277		VAR	1.6e-187	259/277	93	(Shchelkunov *et al.*, 1995)
		303		Rattus norvegicus CD47	3.9e-24	23/86	26	(Nishiyama *et al.*, 1997)
		324		MM integrin assoc. protein	1.0e-21	23/86	26	(Lindberg *et al.*, 1993)
		323		human CD47 precursor	5.0e-19	28/86	32	(Campbell *et al.*, 1992)
150R	138606	83	9.4	**semaphorin-like protein (f1)**				(Kolodkin *et al.*, 1993)
	138857							
A39R		403		VAC	8.0e-46	73/76	96	(Goebel *et al.*, 1990)
A42R		74		VAR-I	8.6e-44	67/71	94	(Shchelkunov *et al.*, 1995)
151R	139163	210	23.9	**semaphorin-like protein (f2)**				(Kolodkin *et al.*, 1993)
	139795							
A39R		403		VAC	3.0-147	209/210	99	(Goebel *et al.*, 1990)
A43R		139		VAR (I:A44R)	1.8e-68	91/105	86	(Shchelkunov *et al.*, 1995)
		653		semaphorin-like protein Alcelaphine herpesvirus	1.7e-20	29/79	36	(Ensser and Fleckenstein, 1995)
				37 matches to semaphorin				

GENOMIC SEQUENCE OF THE MVA STRAIN

ORF[a]	START STOP	AA[b]	kDa[c]	name / (putative) function / homologies[e]	BLAST[d] expect	BLAST[e] AA id	HSS[f] (%)	references
left terminal region:								
				/collapsin gene family				
152R	139821	168	19.4	NK cell receptor homolog				(Scheiflinger et al., unpubl.)
	140327			lectin-like protein				(Smith *et al.*, 1991)
A40R		168		VAC	6.6e-97	134/137	97	(Goebel *et al.*, 1990)
A45R		61		VAR-I (BSH: A43.5R)	9.6e-36	54/59	91	(Shchelkunov *et al.*, 1995)
		233		HS natural killer (NK) cell protein group 2-A, B	4.5e-11	20/74	27	(Houchins *et al.*, 1991)
		240		HS type II membrane protein	6.9e-11	16/36	44	(Adamkiewicz *et al.*, 1994)
		182		MM NK cell receptor	5.5e-09	16/36	44	(Giorda *et al.*, 1992)
		179		HS CD 94	1.7e-07	11/29	37	(Chang *et al.*, 1995a)
				127 matches to lectins including NK cell surface proteins and snake venoms				
153L	141025	219	25.1	25.1k protein				(Smith *et al.*, 1991)
A41L	140366	219		VAC	1.9e-158	218/219	99	(Goebel *et al.*, 1990)
A44L		218		VAR-BSH (I:A46L)	1.4e-152	152/159	95	(Shchelkunov *et al.*, 1995)
		244		VAC B29R/C23L	0.0076	12/53	22	(Goebel *et al.*, 1990)
		258		Rabbit fibroma virus T1	0.057	13/49	26	(Upton *et al.*, 1987)
154R	141197	128	14.5	profilin-like protein				(Blasco *et al.*, 1991)
	141583							(Smith *et al.*, 1991)
A42R		133		VAC	1.2e-87	85/87	97	(Goebel *et al.*, 1990)
A47R		133		VAR-I (BSH:A45R)	1.4e-85	82/87	94	(Shchelkunov *et al.*, 1995)
		140		HS profilin	2.2e-23	19/45	42	(Kwiatkowski and Bruns, 1988)
				10 matches profilin family				
155R	141621	190	22.1	class I membrane				(Smith *et al.*, 1991)
	142193			glycoprotein				(Duncan and Smith, 1992b)
A43R		194		VAC	1.5e-137	162/164	98	(Goebel *et al.*, 1990)
A48R		195		VAR-I (BSH:A46R)	1.9e-128	101/109	92	(Shchelkunov *et al.*, 1995)
		51		HS leukocyte antigen	0.096	7/23	30	X79517
156R	142201	78	8.8	8.8k protein				(Smith *et al.*, 1991)
	142437	78		VAC-WR SalF6R	3.9e-45	78/78	100	(Smith *et al.*, 1991)
		258		rabbit myosin heavy chain	0.00048	13/39	33	A02985
				144 matches to various asp/glu/lys-rich proteins				
157L	143577	346	39.4	3ß-hydroxysterold				(Moore and Smith, 1992)
	142537			dehydrogenase (3ß-HSD)				(Blasco *et al.*, 1991)
A44L		346		VAC	4.5e-249	342/346	98	(Goebel *et al.*, 1990)
A47L		210		VAR-BSH (I: A49L)	1.1e-136	185/195	94	(Shchelkunov *et al.*, 1995)
MC152R		354		MCV subtype 1	8.2e-104	123/272	45	(Senkevich *et al.*, 1996)
		369		FPV	3.1e-83	33/85	38	(Skinner *et al.*, 1994)
				matches to dihydroflavonol reductases, cholesterol dehydrogenases, UDP-galactose-4-epimerases	>2.8e-05			(Baker and Blasco, 1992)

158R	143624	121	13.3	**superoxide dismutase-like protein**				(Blasco *et al.*, 1991) (Smith *et al.*, 1991)
	143989							
A45R		125		VAC	2.1e-82	94/96	97	(Goebel *et al.*, 1990)
A51R		125		VAR-I BSH A48R	1.1e-82	93/96	96	(Shchelkunov *et al.*, 1995)
				117 matches with superoxide dismutase family	<0.027			
159R	143979	241	27.6	**27.6k protein**				(Smith *et al.*, 1991)
A46R	144701	214		VAC	9.6e-167	238/240	99	(Goebel *et al.*, 1990)
A52R		240		VAR-I (BSH: A49R)	5.6e-164	233/240	97	(Shchelkunov *et al.*, 1995)
160L	145465	238	27.6	**27.6k protein**				(Goebel *et al.*, 1990)
J1L	144749	244		VAR	5.1e-146	114/127	89	(Shchelkunov *et al.*, 1995)
A47L		244		VAC	8.2e-135	121/127	95	(Goebel *et al.*, 1990)
				integrin lipid binding motif				(Smith *et al.*, 1991)
161R	145564	204	23.2	**thymidylate kinase**				(Smith *et al.*, 1991)
A48R	146178	204		VAC	5.2e-140	204/204	100	(Goebel *et al.*, 1990)
J2R		205		VAR	1.1e-137	161/165	97	(Shchelkunov *et al.*, 1995)
				16 matches to thymidylate kinase family	<0.49			
162R	146202	162	18.8	**18.8k protein**				(Smith *et al.*, 1991)
A49R	146690	162		VAC	6.0e-106	159/162	98	(Goebel *et al.*, 1990)
J3R		162		VAR	2.4e-103	154/162	95	(Shchelkunov *et al.*, 1995)
163R	146722	552	63.5	DNA ligase				(Kerr and Smith, 1989)
A50R	148380	552		VAC	0.0	547/552	99	(Goebel *et al.*, 1990)
J4R		552		VAR-I	0.0	537/552	97	(Shchelkunov *et al.*, 1995)
		922		HS DNA ligase III	2.1e-235	102/165	61	(Wei *et al.*,)
		559		shope fibroma ligase	9.9e-213	95/200	47	(Parks *et al.*, 1994)
		564		FPV ligase	3.0e-195	101/170	59	(Skinner *et al.*, 1994)
				31 matches mainly to DNA ligase family	<0.029			
164R	148426	310	34.9	**34.9k protein**				(Antoine *et al.*, 1996)
A51R	149358	334		VAC	1.5e-217	267/274	97	(Goebel *et al.*, 1990)
J5R		334		VAR	9.1e-208	251/274	91	(Shchelkunov *et al.*, 1995)

ORF[a]	START STOP	AA[b]	kDa[c]	name / (putative) function / homologies[g]	BLAST[d] expect	BLAST[e] AA Id	HSS[f] (%)	references
left terminal	region:							
				fusion of *A51R/A55R* ORFs				(Antoine *et al.*, 1996)
165R	149416	315	34.8	**hemagglutinin**				(Shida, 1986)
A56R	150363	315		VAC	1.8e-211	312/315	99	(Goebel *et al.*, 1990)
J9R		313		VAR-I(BSH:J7R)	4.3e-178	183/238	76	(Shchelkunov *et al.*, 1995)
		310		raccoonpox	1.5e-91	74/104	71	(Cavallaro and Esposito, 1992)
				124 matches to various proteins	<0.34			
166R	150659	97	11.4	**guanylate kinase (f)**				(Smith *et al.*, 1991)
A57R	150952	151		VAC	3.2e-62	94/97	96	(Goebel *et al.*, 1990)
J10R		151		VAR (BSH:J8R)	2.2e-57	88/97	90	(Shchelkunov *et al.*, 1995)
		198		MM guanylate kinase	4.3e-24	39/91	42	(Brady *et al.*, 1996)
		197		HS guanylate kinase	2.8e-20	35/91	38	(Brady *et al.*, 1996)
				21 matches mainly to guanylate kinases	<0.20			
167R	151103 152005	300	34.3	**serine/threonine protein kinase**				(Howard and Smith, 1989) (Banham and Smith, 1992) (Lin *et al.*, 1992)
B1R		300		VAC	7.1e-215	298/300	99	(Goebel *et al.*, 1990)
B1R		300		VAR-I	2.7e-210	289/300	96	(Shchelkunov *et al.*, 1995)
		283		VAC B12R	4.9e-49	27/53	50	(Goebel *et al.*, 1990)
				100 matches mainly to protein kinase family	<0.00031			
168R	152144	96	11.5	**24.6k protein (f1)**				
B2R	152434	219		VAC	8.5e-38	54/60	90	(Goebel *et al.*, 1990)
		149		histone H2A pea	0.59	16/50	32	P40281
169R	152289	143	16.1	**24.6k protein (f2)**				(Goebel *et al.*, 1990)
B2R	152720	219		VAC	5.7e-86	124/128	96	(Goebel *et al.*, 1990)
170R	152917	179	20.9	**20.9k protein (f)**				
B3R	153456	124		VAC	8.2e-33	51/56	91	(Goebel *et al.*, 1990)
		167		VAC WR	5.3e-45	51/56	91	(Smith *et al.*, 1991)
		92		VAR-GAR H5R	3.4e-06	19/28	67	U18339
171R	153683 154216	177	21.4	**65k ank-like protein virulence factor (f1)**				(Howard *et al.*, 1991) (Mossman *et al.*, 1996)
B4R		558		VAC	8.5e-107	151/154	98	(Goebel *et al.*, 1990)
B6R		558		VAR-I (BSH:B5R)	1.7e-98	140/154	90	(Shchelkunov *et al.*, 1995)
172R	154107 155336	409	47.7	**65k ank-like protein virulence factor (f2)**				(Howard *et al.*, 1991) (Mossman *et al.*, 1996)
B4R		558		VAC	2.4e-283	195/201	97	(Goebel *et al.*, 1990)
B6R		558		VAR-I (BSH:B5R)	2.3e-270	185/201	92	(Shchelkunov *et al.*, 1995)
		483		MYX M-T5 protein	5.5e-10	19/57	33	(Mossman *et al.*, 1996)
		1765		MM ankyrin 3	9.7e-10	22/54	40	(Peters *et al.*, 1995)
		516		orf virus	1.8e-09	16/47	34	U34774
		574		VAC B18R	3.3e-09	11/23	47	(Goebel *et al.*, 1990)
		574		VAR-I B19R	3.6e-09	19/72	26	(Shchelkunov *et al.*, 1995)
		882		HS KIAA0379	5.1e-09	20/52	38	AB002377
		668		CPX host range gene	1.7e-08,	14/47	29	(Spehner *et al.*, 1988)
		237		VAC WR hr gene	2.8e-08	15/47	31	(Kotwal and Moss, 1988a)
		472		VAC M1L	5.1e-07	23/81	28	(Goebel *et al.*, 1990)
		474		CPX O1L	8.7e-07	22/61	36	(Safronov *et al.*, 1996)
		446		VAR O1L	8.8e-07	23/81	28	(Shchelkunov *et al.*, 1995)
		437		CPX D1L	1.7e-06	8/27	29	(Safronov *et al.*, 1996)
		634		VAC C9L	7.8e-05			(Goebel *et al.*, 1990)
				159 matches including ankyrin proteins				

173R	155424	317	35.1	**ps/hr protein/**				(Takahashi-Nishimaki *et al.*, 1991)
	156377			**EEV gp42**				(Engelstad *et al.*, 1992)
				complement control protein				(Isaacs *et al.*, 1992)
B5R		317		VAC	1.6e-232	312/317	98	(Goebel *et al.*, 1990)
B7R		317		VAR-I (BSH:B6R)	7.1e-220	294/316	93	(Shchelkunov *et al.*, 1995)
		259		CPXD17L	2.1e-12	16/52	30	(Safronov *et al.*, 1996)
				186 matches to complement control protein family	<7.7e-05			
174R	156474	173	20.2	**20.2k protein**				
B6R	156995	173		VAC	1.5e-121	173/173	100	(Goebel *et al.*, 1990)
B7R		65		VAR-BSH (I:B8R)	6.0e-40	62/65	95	(Shchelkunov *et al.*, 1995)
		685		NAD-protein ADP ribosyl-transferase phage T4	0.56	17/56	30	SXBPT4
175R	157033	177	20.7	**20.7k protein**				
B7R	157566	182		VAC	7.8e-129	95/108	87	(Goebel *et al.*, 1990)
		184		VACC8L	0.16	9/44	20	(Goebel *et al.*, 1990)
		182		CPXD12L	0.49	8/36	22	(Safronov *et al.*, 1996)
				EF-hand calcium-binding domain				
176R	157621	226	26.0	**31k interferon-gamma**				(Upton *et al.*, 1992)
	158301			**receptor (f)**				(Alcami and Smith, 1995)
B8R		272		VAC	3.3e-164	116/123	94	(Goebel *et al.*, 1990)
B8R		266		VAR-BSH (I:B9R)	3.0e-153	111/123	90	(Shchelkunov *et al.*, 1995)
		266		ECT	2.6e-151	110/123	89	(Mossman *et al.*, 1995b)
		274		swinepox C6	3.2e-09	12/31	38	(Massung *et al.*, 1993)

GENOMIC SEQUENCE OF THE MVA STRAIN

ORF[a]	START STOP	AA[b]	kDa[c]	name / (putative) function / homologies[g]	BLAST[d] expect	BLAST[e] AA id	HSS[f] (%)	references
left terminal region:								
177R	158458	72	8.3	**8.3k protein**				
B9R	158676	77		VAC	3.0e-49	60/60	100	(Goebel *et al.*, 1990)
		240		capripox T4 protein	1.2e-09	16/44	36	M28823
		237		shope fibroma virus	0.0057	15/50	30	F43692
178R	158639	158	17.9	**17.9k protein**				
B10R	159115	166		VAC	4.7e-110	146/146	100	(Goebel *et al.*, 1990)
		530		swinepox VC04	0.040	13/42	30	(Massung *et al.*, 1993)
		689		kelch protein D. melanogaster	0.14	12/54	27	(Xue and Cooley, 1993)
								(Senkevich *et al.*, 1993b)
179R	159187	74	8.5	**8.5k protein**				
B11R	159411	88		VAC	9.2e-43	70/73	95	(Goebel *et al.*, 1990)
				177 matches to glu/asn rich proteins				
180R	159478	283	33.3	**protein kinase**				(Howard and Smith, 1989)
B12R	160329	283		VAC	1.8e-207	282/283	99	(Goebel *et al.*, 1990)
B12R		134		VAR-1	8.7e-26	31/54	57	(Shchelkunov *et al.*, 1995)
		300		VAC B1R	1.7e-54	26/53	49	(Goebel *et al.*, 1990)
		300		VAR-1 B1R	7.7e-53	25/53	47	(Shchelkunov *et al.*, 1995)
				120 matches mainly to protein kinase family	<0.34			
181R	160437 160787	116	13.0	**ICE inhibitor / SPI-2 (f1)**				(Kotwal and Moss, 1989) (Smith *et al.*, 1989)
B13R				VAC				(Ray *et al.*, 1992)
B13R		116		VAR-1 (BSH:B12R)	3.0e-72	111/116	95	(Goebel *et al.*, 1990)
		344		CPX crmA	2.7e-69	105/114	92	(Shchelkunov *et al.*, 1995)
		341		VAC C12L (SPI-1)	2.8e-39	66/100	66	(Pickup *et al.*, 1986)
		353		Ectromelia serpin	2.1e-23	25/34	73	(Goebel *et al.*, 1990)
		344		rabbitpox SPI-1	9.2e-23	24/34	70	(Senkevich *et al.*, 1993b)
		357		CPX SPI-1	5.5e-22	25/34	73	(Ali *et al.*, 1994)
		355		VAR-1 B25R (BSH:B21R)	1.4e-21	25/36	69	(Ali *et al.*, 1994)
		372		CPX serpin-like protein	1.7e-21	25/34	73	(Shchelkunov *et al.*, 1995)
		372		135 matches mainly to serpins	1.7e-36	25/36	69	(Ali *et al.*, 1994)
					<0.12			
182R	160762	222	24.9	**ICE inhibitor/SPI-2 (f2)**				see above
B14R	161430	222		VAC	6.2e-158	218/222	98	(Goebel *et al.*, 1990)
		345		VAC WR	9.4e-156	215/221	97	(Kotwal and Moss, 1989)
		345		rabbit pox SPI-2	1.6e-153	211/221	95	(Ali *et al.*, 1994)
		341		CPX crmA	4.5e-148	203/220	92	(Pickup *et al.*, 1986)
B13R		344		VAR-1 (BSH:B12R)	1.5e-146	203/220	92	(Shchelkunov *et al.*, 1995)
				309 matches see above	<1.3e-21			

183R	161506	143	16.7	**16.7k protein**				(Smith and Chan, 1991)
B15R	161937	149		VAC	3.6e-105	97/98	98	(Goebel *et al.*, 1990)
B14R		149		VAR-I(BSH:B13R)	9.1e-104	95/98	96	(Shchelkunov *et al.*, 1995)
		153		VAR-I DiL (BSH:D2L)	8.8e-31	25/52	48	(Shchelkunov *et al.*, 1995)
		181		VAC C16L/B22R	1.0e-26	25/52	48	(Goebel *et al.*, 1990)
		159		capripox T3A	1.4e-17	17/42	40	(Gershon and Black, 1989a)
		151		rabbit fibroma T3A	2.6e-07	17/44	38	(Upton *et al.*, 1987)
		190		VAC A52R	0.073	10/28	35	(Goebel *et al.*, 1990)
		149		VAC WR K7R	0.21	7/22	31	(Boursnell *et al.*, 1988)
		149		VAR-I C4R	0.30	7/22	31	(Shchelkunov *et al.*, 1995)
		161		CPX M6R	0.51	7/22	31	(Safronov *et al.*, 1996)
184R	162021	326	36.6	**interleukin-1ß receptor (IL-1BR)**				(Alcami and Smith, 1992)
	163001							(Spriggs *et al.*, 1992)
		326		VAC-WR B15R	2.8e-229	323/326	99	(Smith *et al.*, 1991)
		326		CPX B16	2.3e-217	306/326	93	(Spriggs *et al.*, 1992)
B16R		290		VAC	4.4e-202	287/290	98	(Goebel *et al.*, 1990)
B17R		69		VAR-I (BSH:deleted)	8.1e-38	59/68	86	(Shchelkunov *et al.*, 1995)
		296		HS type II IL-1 receptor	1.7e-36	28/75	37	U64094
				271 matches mainly to IL-1 receptors, growth factor receptors and Ig family proteins	<0.011			
185L	164069	340	39.6	**39.6k protein**				
B17L	163047	340		VAC	4.8e-248	335/340	98	(Goebel *et al.*, 1990)
B15L		340		VAR-BSH (I:B18L)	2.7e-241	325/340	95	(Shchelkunov *et al.*, 1995)
186R	164209	574	68.0	**68k ank-like protein**				(Smith *et al.*, 1991)
B18R	165933	574		VAC	0.0	560/574	97	(Goebel *et al.*, 1990)
B19R		574		VAR-I (BSH:B16R)	0.0	539/574	93	(Shchelkunov *et al.*, 1995)
				100 matches mainly to poxvirus ankyrin proteins	<0.53			
187R	165999	234	27.5	**surface antigen, IFN-alpha/beta receptor (f)**				(Ueda *et al.*, 1990)
	166703							(Symons *et al.*, 1995)
								(Colamonici *et al.*, 1995)
B19R		353		VAC (WR:B18R)	1.4e-163	218/233	93	(Goebel *et al.*, 1990)
B20R		354		VAR-I (BSH:B17R)	1.53-149	111/133	83	(Shchelkunov *et al.*, 1995)
		569		HS interleukin-1 receptor	0.0051	15/43	34	(McMahan *et al.*, 1991)
				28 matches mainly to IL-1 receptors	<0.53			
188R	167202	70	8.2	**8.2k protein (f)**				

ORF[a]	START STOP	AA[b]	kDa[c]	name / (putative) function / homologies[g]	BLAST[d] expect	BLAST[e] AA id	HSS[f] (%)	references
left terminal region:								
B22R	167414	1897		VAR-BSH (I:B26R)	9.9e-23	31/38	81	(Shchelkunov *et al.*, 1995)
189R	167897	188	21.7	21.7k protein				
B22R	168463	181		VAC B22R/C16L	2.9e-111	95/104	91	(Goebel *et al.*, 1990)
D1L		153		VAR-I (BSH:D2L)	1.2e-88	66/71	92	(Shchelkunov *et al.*, 1995)
		149		VAC B15R	7.2e-19	25/52	48	(Goebel *et al.*, 1990)
		159		capripox T3A	8.0e-05	15/45	33	(Gershon and Black, 1989a)
		151		VAC C6L	0.25	12/46	26	(Goebel *et al.*, 1990)
		156		VAR (I:D9L;BSH:D12L)	0.26	12/46	26	(Shchelkunov *et al.*, 1995)
190R/	168531	233	26.9	45k ank-like protein				
004L	169232			(f2)				
B23R		386		VAC (C17L/B23R)	6.2e-159	110/110	100	(Goebel *et al.*, 1990)
D1L		91		VAR-BSH	9.1e-31	46/49	93	(Shchelkunov *et al.*, 1995)
		669		CPX host range	1.1e-13	22/50	44	(Spehner *et al.*, 1988)
		452		VAR-I D6L (BSH:D8L)	1.7e-11	21/50	42	(Shchelkunov *et al.*, 1995)
		574		VAR-I B19R (BSH: B16R)	1.2e-05	22/73	30	(Shchelkunov *et al.*, 1995)
		574		VAC B18R (WR: B17R)	8.6e-05	22/73	30	(Goebel *et al.*, 1990)
		634		VAC C9L	0.00011	11/24	45	(Kotwal and Moss, 1988a)
		585		VAR-I G1R	0.00013	22/74	29	(Shchelkunov *et al.*, 1995)
		516		orf virus	0.0088	15/49	30	(Sullivan *et al.*, 1995b)
		153		VAR-I D7L (BSH:D10L)	0.014	12/28	42	(Shchelkunov *et al.*, 1995)
191R/	169309	102	12.1	45k ank-like protein				
003L	169617			(f1)				
B23R		386		VAC C17L/B23R	1.3e-39	62/63	98	(Goebel *et al.*, 1990)
192R/	170305	176	19.7	secr. TNF receptor (f)				(Upton *et al.*, 1991a)
002L	170835	355		CPX crmB	5.1e-71	76/83	91	(Hu *et al.*, 1994)
G2R		348		VAR-BSH	1.0e-66	73/83	87	(Shchelkunov *et al.*, 1995)
		326		Myxoma virus T2	4.9e-30	21/37	56	(Upton *et al.*, 1991a)
		325		Rabbit fibroma Virus T2	1.8e-28	17/36	47	(Upton *et al.*, 1987)
		202		CPX C4L	8.7e-15	30/51	58	(Heller *et al.*, 1990)
B25R		346		HS TNF receptor	1.9e-08	14/26	53	(Safronov *et al.*, 1996)
		259		VAC (*C19L/B25R*)	0.00026	16/19	84	(Goebel *et al.*, 1990)
		277		human CD40L receptor	0.0015	11/24	45	(Stamencovic *et al.*, 1989)
				30 matches to TNF receptors and surface proteins	<0.39			
193R/	171267	136	14.9	35k major secr. protein				(Patel *et al.*, 1990)
001L	171677			chemokine receptor (f)				(Graham *et al.*, 1997)
B29R		244		VAC (*C23L/B29R*)	6.0e-57	41/42	97	(Goebel *et al.*, 1990)
G5R		253		VAR-I	8.9e-51	46/49	93	(Shchelkunov *et al.*, 1995)
		246		CPX ORF B	5.6e-49	40/42	95	(Hu *et al.*, 1994)
		258		SFV T1 protein	2.5e-20	23/42	54	(Upton *et al.*, 1987)
		260		Myxoma virus T1/35kDa	1.5e-14	21/42	50	(Graham *et al.*, 1997)

[a] Open reading frame coding for at least 65 amino acids (for exceptions see text); minor ORFs located in reverse orientation within large ORFs or ORFs located in the repeat regions of the ITRs (see text) are not listed; the MVA ORFs (boldface), listed consecutively as appearing in the genome, and homologs in the Copenhagen strain (in italics), in the variola strains and in the molluscum contagiosum, are listed in this row. Split ORFs are boxed.

[b] Number of deduced amino acids (AA) encoded within an ORF.

[c] Predicted M_r (kDa) for the unmodified protein.

[d] The lowest Poisson probability determined by the BLAST search (Altschul *et al.*, 1990). The Expect value of 0.0 indicates a probability of zero that an alignment occurs by chance; low Expect values correspond to high homology and vice versa.

[e] Amino acid identity (AA id) of first high-scoring segment pair in the BLASTp protocol.

[f] Amino acid identity of first high-scoring segment pair (HSS)%.

[g] Homologies based on searching PIR and SWISS-PROT databases (BLASTp nr).

[h] Duplicated ORFs located in ITRs.

[i] Fragment; complete homologous ORF present in related poxvirus (see reference).

[j] Variola India (I) or variola Bangladesh (BSH) sequences; in cases where the variola sequences are not identical, the variola strain first appearing in the blast search protocol is listed.

[k] ank, ankyrin.

[l] HS, homo sapiens.

[m] MM, *Mus musculus*.

Please **REPLACE** References, pages 46-53, in the specification as follows:

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